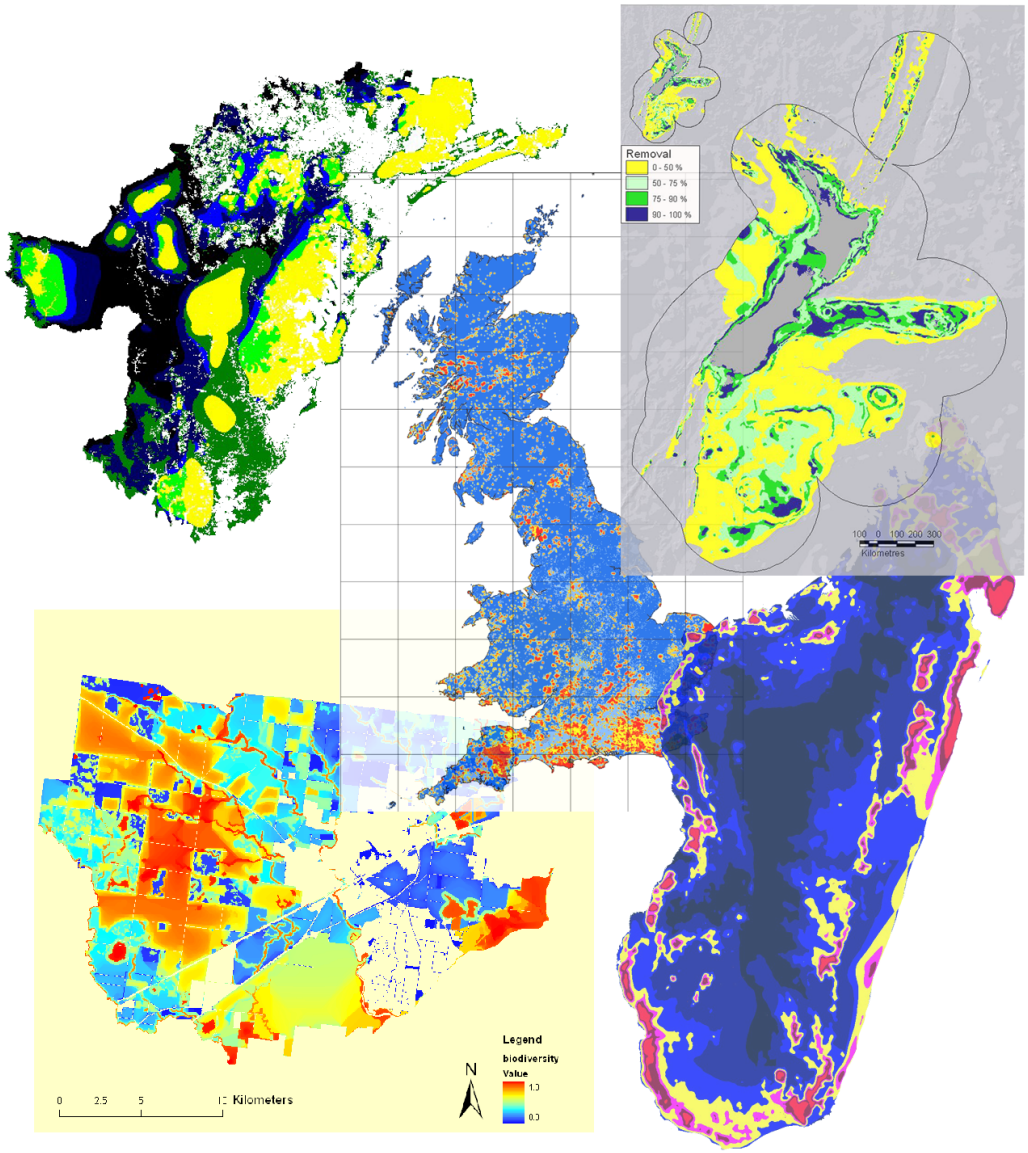
ZONATION

Spatial conservation planning framework and software v. 1.0

User Manual

Atte Moilanen & Heini Kujala



© 2004-2006 Atte Moilanen

Zonation

Software for spatial conservation planning

---

by Atte Moilanen

Zonation is a reserve selection framework for large-scale conservation planning. It identifies areas, or landscapes, important for retaining connectivity for multiple species, thus providing a quantitative method for enhancing species' long term persistence.

Essentially, this software is a decision support tool for all non-commercial parties working on conservation issues.

Zonation - User manual

© 2004-2006 Atte Moilanen

All rights reserved. USE THIS SOFTWARE AT YOUR OWN RISK. THE AUTHOR WILL NOT BE LIABLE FOR ANY DIRECT OR INDIRECT DAMAGE OR LOSS CAUSED BY THE USE OF THIS SOFTWARE.

CONDITIONS OF USE: Zonation v1.0 is freely usable for non-commercial uses. For any other kinds of uses, contact the author for permission.

Do not use this software if you disagree with the disclaimer and conditions of use.

Even though the ZIG software has been done with the best of intentions, it is quite beyond one researcher to ensure its correct operation under all operating systems and environments. Also anticipating and checking for all combinations of erroneous input has not been possible. Therefore, use the software with care and make an effort to understand the output and make a reality check as to whether the results make logical sense.

Printed: 2006 in Helsinki, Finland

Publisher
Atte Moilanen/ Metapopulation Research Group

Managing Editor
Atte Moilanen

Technical Editors
Heini Kujala
Anni Arponen

Cover Designer
Heini Kujala
Atte Moilanen

Cover Photo
Evgeniy Meyke

Special thanks to:

Anni Arponen, Alison Cameron, Aldina Franco, Ascelin Gordon, John Leathwick, Grzegorz Mikusinski, Chris Thomas and Brendan Wintle are thanked for comments on the software and its functions and usability.

Thenk's to Anni Arponen who helped with an early version of Zonation documentation, and many thanks to Mar Cabeza, who commented the first version of the manual. Brendan Wintle generously provided sample data files from the Hunter Valley region, and Evgenyi Meyke kindly provided beautiful background photographs for the Zonation documentation.

Thank's to all who have collaborated in the development of Zonation methods and applications.

This work was supported by the Academy of Finland project 1206883 to the author, and two Academy of Finland Centre of Excellence grants (2000-2005 and 2006-2011) to the MRG lead by Academy professor Ilkka Hanski.

Helsinki, November 22, 2006

Atte Moilanen
Academy Research Fellow
Metapopulation Research Group
Dept. Biological and Environmental Sciences
P.O. Box 65
FI-00014 University of Helsinki
Finland

Table of Contents

Part I Introduction 4

1 Aim & purpose ... 4
2 The Zonation framework ... 5
3 Zonation compared to other reserve selection approaches ... 5
Zonation ... 5
Integer programming ... 6
Stochastic global search ... 6
4 A typical Zonation work flow ... 7
5 Software installation and quick start ... 8

Part II Methods & algorithms 12

1 References ... 12
2 The Zonation meta-algorithm ... 13
3 The cell removal rule ... 14
Basic core-area Zonation ... 14
Additive benefit function ... 15
Target-based planning ... 16
General differences between cell removal rules ... 17
4 Inducing reserve network aggregation ... 19
Distribution smoothing ... 20
Boundary Quality Penalty (BQP) ... 21
Boundary Length Penalty (BLP) ... 23
5 Uncertainty analysis ... 24
Uncertainty in species distributions, distribution discounting ... 25
Uncertainty in the effects of landscape fragmentation ... 27
6 Replacement cost analysis ... 28
7 Assumptions & limitations ... 31

Part III ZIG - The Zonation software 33

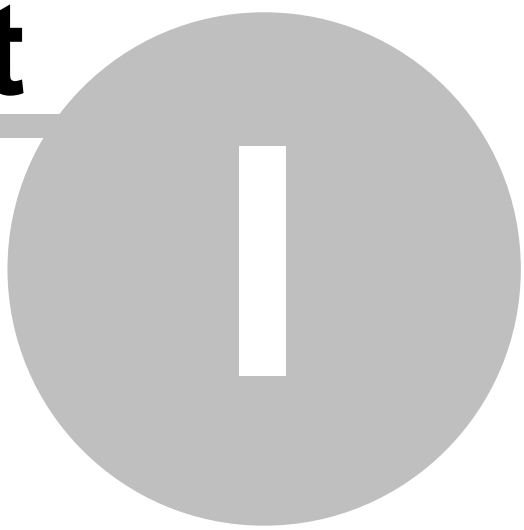
1 Introduction ... 33
2 Running Zonation ... 33
Command prompt ... 33
Windows interface ... 34
Batch-run capability ... 35
Loading previously calculated Zonation solutions ... 37
3 Input files & settings ... 37
Introduction ... 37
Compulsory files ... 38
Species distribution map files ... 38
Species list file ... 39
Run settings file ... 42
Optional files ... 45
Cost layer ... 45
Removal mask layer ... 46
Distributional uncertainty map layer ... 47

© 2004-2006 Atte Moilanen

Uncertainty analysis weights file ... 48
Boundary quality penalty definitions file ... 48
4 Standard Zonation output ... 50
Visual output ... 50
Automated file output ... 55
5 Main analyses ... 57
Basic Zonation and species weighting ... 57
Distribution smoothing + Zonation ... 59
BQP Zonation ... 61
Including distributional uncertainty - Distribution discounting ... 63
Inclusion/Exclusion cost analyses using mask files ... 66
6 Post-processing analyses & options ... 69
Landscape identification ... 69
Statistics for management landscapes ... 72
Solution comparison ... 73
Fragmentation uncertainty anlysis ... 75
ZIG_Sum Utility ... 77
Solution cross-comparison using solution loading ... 80
7 Tips for using the command prompt ... 81
8 Troubleshooting ... 81
9 Assumptions, limitations & system requirements ... 83
10 Known software problems and bugs ... 83
Part IV Tutorial & Examples 85
Index 101

© 2004-2006 Atte Moilanen

Part



1 Introduction

1.1 Aim & purpose

Zonation is a reserve selection framework for large-scale spatial conservation planning. It identifies areas, or landscapes, that are important for retaining habitat quality and connectivity for multiple species, thus providing a quantitative method for enhancing species' long term persistence.

Zonation produces a hierarchical prioritisation of the landscape based on the biological value of sites (cells). The algorithm proceeds by removing least valuable cells from the landscape one at a time while minimizing the loss rate of biodiversity and connectivity. As a result, a nested sequence of highly connected landscape structures is obtained with the core areas of species distributions remaining latest and previously-removed areas showing as buffer zones. In this way, landscapes can be zoned according to their potential for conservation, and differing degrees of protection can be applied to different zones. The purpose is not necessarily to produce a detailed conservation plan for a large region, but to identify priority areas of the landscape that could be subjected for more detailed analysis and planning that accounts for other land-use pressures than nature conservation.

The Zonation software has been geared towards using large grids as input data. Thus, it is particularly simple to input modelled species distributions (or land cover types) into Zonation. First do statistical habitat models for species, then predict species occurrence across the landscape grid, then feed the grids into Zonation. The Zonation software can be run with relatively large datasets on an ordinary desktop PC.

The Zonation software is intended for the analysis of biological data with the aim of finding out spatially good conservation solutions. In this process Zonation purposefully ignores other land use planning considerations, such as commercial or recreational values (except for what can be entered as simple cost/mask layers). Thus, output of Zonation should be seen as an analysis of conservation value which feeds into a broader land use planning framework where political decisions are made that balance between different land use needs.

© 2004-2006 Atte Moilanen

1.2 The Zonation framework

Aim and purpose

- To provide a tool for large-scale high-resolution spatial conservation planning using GIS grid data

Analyses

- Identification of optimal reserve areas
- Replacement cost analysis for current or proposed reserves

Data

- Large-scale grids with
  - Presence/absence -data
  - Probabilities of occurrence
  - Abundance/density -data
  - Cost layers

Features

- Aggregation methods
  - Distribution Smoothing
  - Boundary Quality Penalty
  - Boundary Length Penalty
- Uncertainty analysis based on information-gap decision theory
- Species weighting
- Planning methods
  - Core-area Zonation
  - Additive benefit function
  - Target-based benefit function

1.3 Zonation compared to other reserve selection approaches

In this section we comment on the differences between Zonation and other commonly used approaches to reserve selection. This comparison is not meant to be exhaustive nor completely referenced, but rather, to give an indication of the most fundamental differences (that we believe to exist) between these methods.

1.3.1 Zonation

Input data. Zonation is targeted for use with large grid-based data sets. This implies that species distributions, used within Zonation, might be produced using some predictive statistical technique using environmental layers as predictors for species presence/abundance. Data sets in the order of millions of grid cells can be analyzed.

Output. Instead of outputting the optimal set of sites for achieving targets, Zonation outputs (1) the hierarchy of cell removal throughout the landscape and (2) species loss curves. This kind of output has multiple advantages.

(i) The result for a range of targets is immediately obvious,
(ii) there is an indication of the importance of all cells, both inside and outside any given fraction,
(iii) the curves show how well (relatively) individual species do at any given fraction of the landscape, and
(iv) the curves indicate the relative value of the solution as well as the stability of the solution.

We will elaborate the item (iv). If species performances are declining rapidly at the chosen landscape fraction, it means that the solution is not stable with respect to uncertainty in input data, and that smallish changes in the selected fraction and / or spatial pattern might have large consequences for species. If the species performances are stable at the chosen fraction, then small changes in the fraction/spatial pattern are unlikely to have any significant effect on the solution quality.

© 2004-2006 Atte Moilanen

Optimality. The optimality characteristics of Zonation have not been conclusively examined, but this is our present evaluation of this issue.

(i) Zonation using additive benefit functions or the targeting benefit function (above the target) is very close to globally optimal. This is because with these cell removal rules the optimization problem is convex and can thus be solved using a gradient-like iterative heuristic. (This optimality argument is supported by an as of yet unpublished investigation by van Teefelen and Moilanen). Also, with the additive cell removal rules the degree of suboptimality goes down when the landscape size (number of cells) increases. Thus optimality is not a problem with the additive cell removal rules. Except, use of the BQP renders the problem non-convex (especially if some species benefit from fragmentation), and the degree of sub-optimality of the solution is unknown.

(ii) The core-area Zonation. This method has so far only been defined algorithmically, not in an objective function form, and the degree of suboptimality of results is unknown. Then again, no other implementation of this method is available.

1.3.2 Integer programming

Input data. Can accept arbitrary sites as well as grid cells. According to a relatively recent review, Williams et al. (2004), the data size limits of IP were at that time around 10000 landscape elements, which as a grid is only 100x100 elements. This is orders of magnitude less than the data limits of Zonation, which can run landscapes of 10+ millions of elements even when using the Boundary Quality Penalty.

Output. Globally optimal set of sites achieving targets. No prioritization through the landscape, no performance curves.

Optimality. Guaranteed globally optimal solution to a simplified problem. The value of the global optimality of results is compromised by the requirement that both the objective function and constraints need to be linear (or that they can be linearized). In a sense you have the optimal solution to the wrong (simplified) problem. Not applicable, at least not easily, to BQP calculations on large landscapes.

Williams, J., C.S. ReVelle, and S.A. Levin. 2004. Using mathematical optimization models to design nature reserves. Frontiers in Ecology and the Environment 2:98–105.

1.3.3 Stochastic global search

Stochastic global search includes techniques such as simulated annealing (SA; as in MARXAN) and genetic algorithms (GAs).

Input data. In principle can be run on extremely large problems with few constraints on the complexity of the problem. SA can handle larger problems than a GA, because of the memory requirement for storing the GA population.

Output. A solution to the problem, typically of unknown quality. In some cases it may be possible to devise an analytical method that provides bounds on solution quality (as in Moilanen 2005), which then changes the method from a heuristic to an approximation. (Heuristic = method for which the quality of results is unknown; approximation = method for which the maximum degree of suboptimality of the results has been quantified in a non-trivial manner.)

Optimality. Degree of suboptimality will be highly dependent on (1) the size of the data, (2) the complexity of the problem, like does it have nonlinear connectivity components in it, and (3) the details of the implementation of the optimization algorithm. SA and GA are no way standard algorithms (except for the high-level meta-algorithm). They can be varied in endless ways, in particular, in terms of how they generate the new solutions to evaluate. If search starts far from the good regions of the search space, it actually is not guaranteed that the good regions are found at all. Good convergence with large problems absolutely is not guaranteed. Multiple runs from different starting points are required to test for indications of convergence – and if multiple runs reliably converge to a very similar result, then this indeed is an indication that the solution probably

© 2004-2006 Atte Moilanen

is quite acceptable in terms of optimality. Probably are ok with smallish data sets with thousands or tens of thousands of sites, but at the million-element scale the performance of these methods is poorly known. Relative performance probably degrades when problem size increases, which is opposite from what is actually expected for Zonation, at least with the additive cell removal rules.

There are piles of literature on optimization, which is an enormous field of science in itself. See the references below for examples of the use of stochastic optimization on nonlinear reserve selection problems. Also check MARXAN reserve selection software user manual and references therein.

Moilanen, A. 2005. Reserve selection using nonlinear species distribution models. American Naturalist 165: 695-706. AND in particular its electronic appendixes A-C.

Moilanen, A. and M. Cabeza. 2002. Single-species dynamic site selection. Ecological Applications 12: 913-926.

For a more philosophical intro to these optimization methods see

Moilanen, A. 2001. Simulated evolutionary optimization and local search: Introduction and application to tree search. Cladistics 17:512-525.

1.4 A typical Zonation work flow

This section outlines a typical sequence of steps that would be done for the Zonation analysis of one data set.

(i) Get the basic analyses running

i.1. Install Zonation, and get the basic zonation running with the example files provided.

i.2. Decide your cell removal rule.

i.3. Produce a new settings file, species list file etc. for your own data and check that you are able to run the basic analysis (without aggregation methods or uncertainty analysis).

i.4. Try variants of the basic analysis by adding unequal species weights, aggregation methods and uncertainty analysis. You can use solution comparison to check how big a difference does the addition of one complication cause into the solution. These preliminary analyses can as well be run using high warp-factors (100-1000) to reduce runtimes.

(ii) Identify your base-analysis. There are endless options of what species weights to give, what species-specific parameters exactly to use in the aggregation method (distribution discounting or boundary quality penalty) and what parameter(s) to use in the uncertainty analysis. You cannot run all combinations of everything and indeed it is not useful to do so. Therefore, after getting the basic Zonation running, you need to decide the most reasonable options for your analysis. These options would depend on the availability of data and on your planning needs. Things that need to be decided include

ii.1 Decide species weights. Equal weights is the basic option but there may well be good reason to favour particular species by giving them more weight.

ii.2 Decide about how to induce aggregation into the final solution. Options include distribution smoothing, boundary quality penalty and boundary length penalty. In general, you want aggregation at least if your planning units are small, like hectares or so, because with small selection units population dynamics of nearby cells are strongly linked. If planning units are very large, like 10x10km cells, then aggregation could plausibly be omitted.

ii.3 Decide if some amount of distribution discounting uncertainty analysis would be appropriate.

(iii) Base-analysis and sensitivity analysis. At this point you have identified the analysis options

© 2004-2006 Atte Moilanen

which you believe to be most appropriate. Next

iii.1 Run your base-analysis, preferably using a relatively low warp factor.

iii.2 Run variants around your base-analysis varying a single analysis feature at a time (you probably cannot run all combinations of everything). This is essentially a sensitivity analysis, which is done by varying weights, aggregation and uncertainty analysis settings within reasonable bounds. Investigate using solution comparison how big a difference various options make.

iii.3 An analysis of selection frequency (with ZIG_Sum utility) may provide useful summary information over analyses.

At this point you have a good idea of how different planning options influence your analysis and solutions.

(iv) Identification of reserve areas. Identify management landscapes and check their statistics to find out why different areas are important – what are the biodiversity features that occur there?

(v) Evaluation of proposed reserve areas using replacement cost analysis. If you need to evaluate proposed or existing reserve areas, you can do that using mask files and replacement cost analysis. This involves repeating your base analysis both with and without existing/proposed areas included/excluded.

1.5 Software installation and quick start

Installation

The installation package includes the Zonation program (zig2.exe), the ZIG_Sum utility (zig_sum.exe), a user manual (pdf) and tutorial files. You can find the installation package via the Metapopulation Research Group website:

www.helsinki.fi/science/metapop

For practicality reasons it is recommended to keep data files (including the tutorial) in the same directory with the program! One option is to make a copy of the program to the directory containing data files when starting a new project.

Quick start

Here are instructions to run the basic Zonation for those who have already familiarized themselves, at least to some extend, with the program. For more detailed instructions and additional analyses please see sections 3.2 Running Zonation, 3.3 Input files & settings, 3.5 Main analyses and 3.6 Post-processing analyses & options.

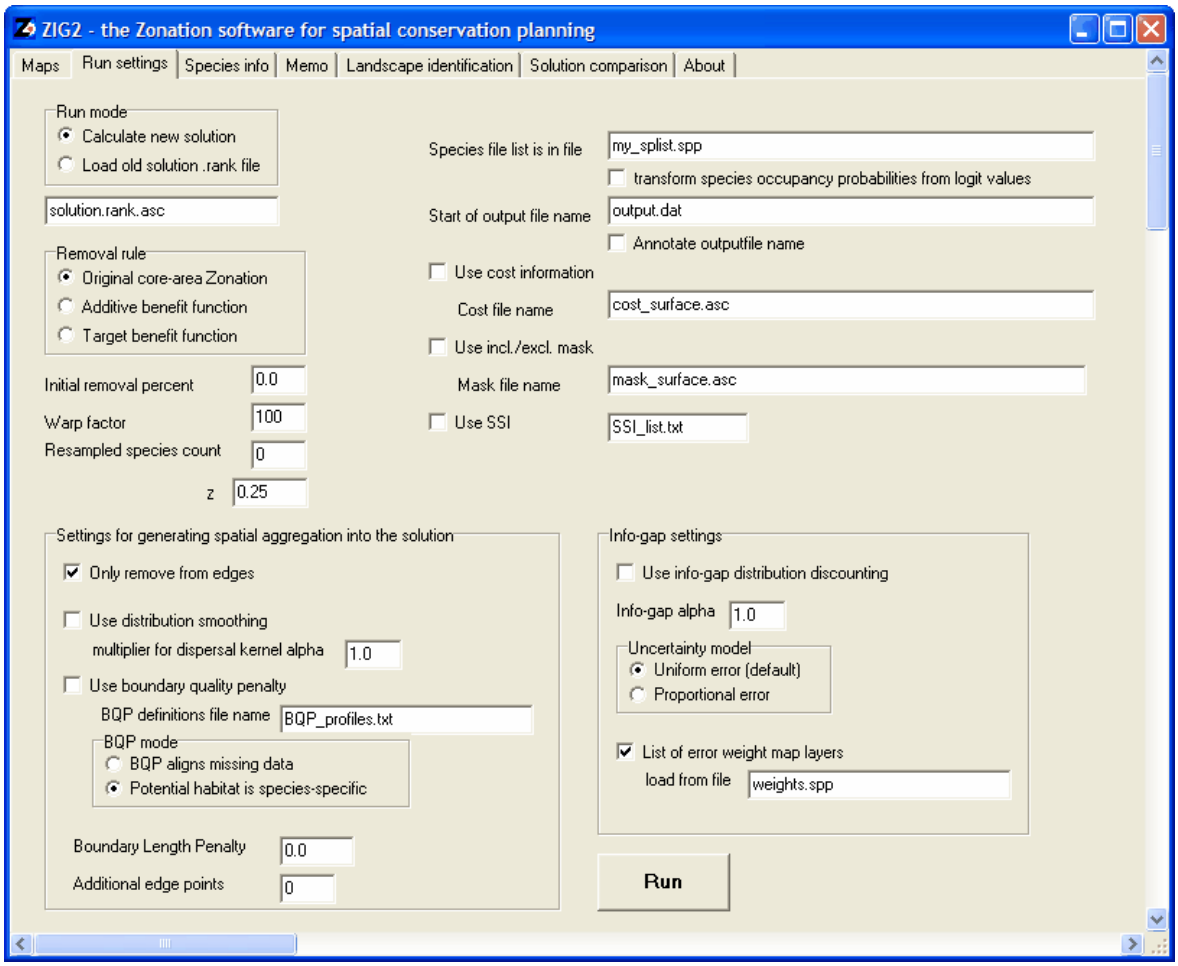
Using Windows interface

1. To run the program you need at least two sets of **input files**:
   - Species distribution map files, which are basic raster files (.asc) exported from GIS programs. These files define species distributions in the landscape. The program can incorporate any kind of species distribution data, such as presence-absence, probabilistic or abundance data, or species-specific population connectivity surfaces etc., as longs as data for all species is in the same format.
   - The names of all the species files must be listed in a separate species list file (.spp), each file on a separate row with the species-specific parameters before the file name (see section 3.3.2.2 Species list file for more detailed descriptions). The species list file tells the program which species distribution files will be used in the analysis.

   Remember to always use decimal points, NOT commas, in all input files!

© 2004-2006 Atte Moilanen

2. Double clicking on the **zig2.exe** icon starts the windows version of the program.
3. Go to **Run settings** **-window** and give the name of your species list file.
4. Select the suitable **cell removal rule**.
5. Give the name of your species list file.
6. Define the name of your **output files**.
7. Press **Run -button** to initiate the computation.
8. For additional settings and analysis see sections 3.3.2.3 Run settings file and 3.5 Main analyses. Features you might consider changing include the warp factor, the uncertainty analyses and the aggregation methods.



Using command prompt

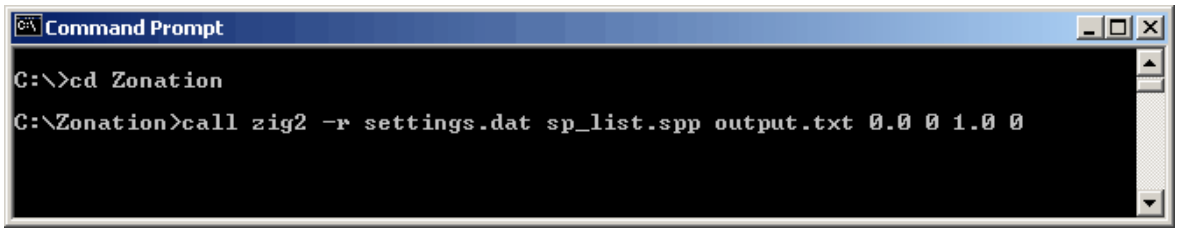
1. To run the program from command prompt, in addition to species distribution map files and species list file you need a third **input file** called run settings file. This will define the setting of your analysis.
2. Select the suitable **cell removal rule** in your run settings file .
3. Open the command prompt from your Windows "Start" -menu.
4. Use "`cd directory_name`" -command to change to the correct working directory which contains the zig2.exe and all the input and settings files. See section 3.7 for

© 2004-2006 Atte Moilanen

working with the command prompt.

5. Call the program with the following command line:
   ```
   call zig2 -r settingsfile.dat specieslistfile.spp outputfile.txt
   0.0 0 1.0 0
   ```
   In this command line, give the names of your settings file and species list file and define a suitable name for your output files. See section 3.2.1 for explanations for the four numbers in the call.

6. Press enter to initiate the computation.



The basic Zonation program can be used for example for identifying a best proportion of the landscape (rank selection in Map window), or for identifying the area required for representing a certain proportion of the species' distributions (proportional selection in Map window).

The program automatically produces five output files:

- .jpg and .bmp maps of the landscape ranking showing the order cell removal in different colours. See section 3.4.1 for detailed interpretation of the colours.
- A .curves.txt -text file containing a list of species and weights used in the analysis, and columns representing how large proportion of distribution of each specie is remaining when landscape is iteratively removed.
- A .rank.asc -raster file representing the order of cell removal (ranking). This file can be used to produce map images in GIS softwares.
- A .prop.asc -raster file representing proportions of species distributions (across species) remaining at the removal of that cell. This file can be used to produce map images in GIS softwares.
- A .run_info.txt -text file copy of the **Memo**. This file will be created after you have closed the program.

For saving other results (pictures of specific maps or curves), double click on the map image. See also examples on visual output.

© 2004-2006 Atte Moilanen

Part II

2 Methods & algorithms

2.1 References

The basic Zonation analysis and distribution smoothing

Moilanen, A., Franco, A. M. A., Early, R., Fox, R., Wintle, B., and C. D. Thomas. 2005. Prioritising multiple-use landscapes for conservation: methods for large multi-species planning problems. Proceedings of the Royal Society of London, Series B, Biological Sciences 272: 1885-1891.

Moilanen, A. 2007. Landscape zonation, benefit functions and target-based planning: Unifying reserve selection strategies. Biological Conservation, in press, corrected proofs available online - doi:10.1016/j.biocon.2006.09.008.

Distribution smoothing, info-gap uncertainty analysis

Moilanen, A. and B. A. Wintle. 2006. Uncertainty analysis favours selection of spatially aggregated reserve structures. Biological Conservation 129: 427-434.

Basics of the information-gap decision theory for reserve selection uncertainty analysis

Moilanen, A., Runge, M. C., Elith, J., Tyre, A., Carmel, Y., Fegraus, E., Wintle, B., Burgman, M. and Y. Ben-Haim. 2006a. Planning for robust reserve networks using uncertainty analysis. Ecological Modelling 199: 115-124.

Accounting for distributional uncertainty, the distribution discounting method

Moilanen, A., B. A. Wintle, J. Elith and M. Burgman. 2006b. Uncertainty analysis for regional-scale reserve selection. Conservation Biology 20: 1688-1697.

A quantitative method for generating reserve network aggregation

Moilanen, A., and B. A. Wintle. 2007. The boundary-quality penalty: a quantitative method for approximating species responses to fragmentation in reserve selection. Conservation Biology, in press.

Replacement cost analysis

Cabeza, M. and A. Moilanen. 2006. Replacement cost: a useful measure of site value for conservation planning. Biological Conservation 132: 336-342.

See also the following references for the benefit function approach to reserve selection

Arponen, A., Heikkinen, R., Thomas, C.D. and A. Moilanen. 2005. The value of biodiversity in reserve selection: representation, species weighting and benefit functions. Conservation Biology 19: 2009-2014.

Arponen, A., Kondelin, H. and A. Moilanen. (2007). Area-Based Refinement for Selection of Reserve Sites with the Benefit-Function Approach. Conservation Biology, in press, corrected proofs available online - doi: 10.1111/j.1523-1739.2006.00607.x.

For those who would wish to familiarize themselves more broadly with recent literature concerning spatial conservation planning, we recommend using Web of Science (or a similar search facility) with key words such as, **reserve selection**, **reserve network design**, **site selection algorithm**, **area prioritisation**, **spatial conservation planning** and **spatial optimisation**.

© 2004-2006 Atte Moilanen

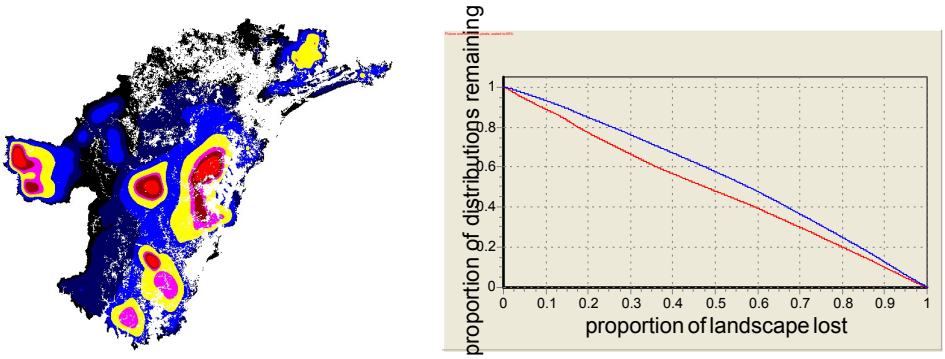
2.2 The Zonation meta-algorithm

The Zonation algorithm (Moilanen et al. 2005) produces a hierarchical prioritization of the conservation value of a landscape, hierarchical meaning that the most valuable 5% is within the most valuable 10%, the top 2% is in the top 5% and so on. At a high level, Zonation simply iteratively removes cells one by one from the landscape, using minimization of marginal loss as the criterion to decide which cell is removed next. The order of cell removal is recorded and it can later be used to select any given top fraction, like best 10%, of the landscape. Simultaneously, information is collected about the decline of representation levels of species during cell removal.

The Zonation meta-algorithm

1. Start from the full landscape. Set rank r = 1.
2. Calculate marginal loss following from the removal of each remaining site i, δ_i.
3. Remove the cell with smallest δ_i, set removal rank of i to be r, set r=r+1, and return to 2 if there are any cells remaining in the landscape.

Thus, sites are ranked based on biological value and the least valuable cells are removed one (or more) at a time, producing a sequence of landscape structures with increasingly important biodiversity features remaining. It is emphasized that the result of a Zonation analysis is not a single set of areas. Rather, it is (i) the nested ranking of cells and (ii) a set of performance curves describing the performance of the solution at the given level of cell removal.



Sample figures illustrating the ranking and the curves.

The Zonation meta-algorithm can, among other things, answer two questions frequently encountered in conservation biology:

- which parts of the landscape, totalling x% of landscape cost or area, have the highest conservation priority (ranking), or,
- which part of the landscape includes at least y% of the distribution of each species (proportional coverage selection)?

Whether the Zonation algorithm makes any sense at all depends on the definition of marginal loss (δ_i), step 2 in the algorithm above. This definition is done by a separate cell removal rule, which is described in the next chapter (see 2.3.). The Zonation method can thus be divided into two parts, the Zonation meta-algorithm and the cell removal rule, which should not be confounded. The cell removal rule should be seen as a separate component with several alternatives that have different interpretations. Note that the notion of complementarity is inherent in the way the cell removal rule is defined.

There is one feature, which according to Moilanen et al. (2005) is a part of the Zonation algorithm, but which is more appropriately seen as a relevant detail for which there are alternatives. This is edge removal, by which it is meant that cells can only be removed from the edge of the remaining landscape. Edge removal may promote maintenance of structural habitat continuity in the removal process. It also makes the cell removal process much faster with large landscapes, which is the primary reason for using it.

© 2004-2006 Atte Moilanen

2.3 The cell removal rule

This section is mainly based on Moilanen 2007 - *Landscape Zonation, benefit functions and target-based planning: unifying reserve selection strategies* (*Biol. Conserv.*, in press, corrected proofs available online).

The Zonation meta-algorithm is the same for all analyses described in this manual. The rule that determines which cell has the lowest biological value, and is therefore removed next, differs depending on the cell removal rule that is chosen. There are three conceptually different cell removal rules:

1. Core-area Zonation
2. Additive benefit function
3. Target-based planning

We first describe the different cell removal rules and the theory behind them, and then highlight the main differences between the rules and give some guide lines how to choose the most suitable one for your analysis.

Note that core-area Zonation has the property that it can identify species-poor locations where a single species has an important occurrence. The additive benefit function analysis gives more weight to locations with high species richness. Therefore, it may be useful to run both analyses and compare results. If the top-fractions do not agree, then there are some species-rich areas but also some species-poor areas with occurrences of otherwise rare species. Thus running both core-area Zonation and the additive benefit function analysis may reveal information that is interesting for conservation planning.

2.3.1 Basic core-area Zonation

This section is mainly based on Moilanen *et al.* (2005) and Moilanen (2007).

In basic core-area Zonation cell removal is done in a manner that minimizes biological loss by picking cell *i* that has the smallest value for the most valuable occurrence over all species in the cell. In other words, the cell gets high value if even one species has a relatively important occurrence there. The removal is done by calculating a removal index δ_i (minimum marginal loss of biological value) for each of the cells, where:

$$\delta_i = \max_j \frac{Q_{ij}(S) w_j}{c_i}, \qquad (1a)$$

where w_j is the weight (or priority) of species *j* and c_i is the cost of adding cell *i* to the reserve network. When running the analysis the program goes through all cells and calculates them a value δ_i based on that species that has the highest proportion of distribution remaining in the specific cell (and thus represents the highest biological value to be lost, if the cell is removed). The cell which has the lowest δ_i -value, will be removed.

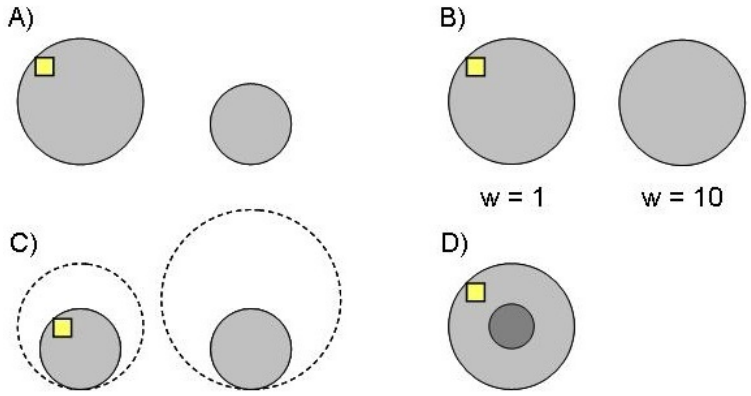
The critical part of the equation is $Q_{ij}(S)$, the proportion of the remaining distribution of species *j* located in cell *i* for a given reserve network *S*. When a part of the distribution of a species is removed, the proportion located in each remaining cell goes up. This means that Zonation tries to retain core areas of all species until the end of cell removal even if the species is initially widespread and common. Thus, at first only cells with occurrences of common species are removed. Gradually, the initially common species become more rare, and cells with increasingly rare species occurrences start disappearing. The last site to remain in the landscape is the cell with the highest (weighted) richness. This is the site that would be kept last if all else was to be lost. Note that Eq. (1a) can alternatively be expressed as (Moilanen et al. 2005)

$$\delta_i = \max_j \frac{q_{ij}(S) w_j}{Q_j(S) c_i}, \qquad (1b)$$

© 2004-2006 Atte Moilanen

where q_{ij} is the fraction of the original full distribution of species *j* residing in cell *i* according to data, and $Q_j(S)$ is the fraction of the original distribution of species *j* in the remaining set of cells *S*.

The min-max structure of the equation also indicates a strong preference to retaining the best locations with highest occurrence levels. Thus, the program can spare otherwise species-poor cells, if they have a very high occurrence level for one rare species. It is important to understand that core-area Zonation does not treat probabilities of occurrence as additive; ten locations with p=0.099 is not the same as one location with p=0.99. However, this is strictly true only when analysis is based on biological value only and when a landscape cost layer is not used in the analysis. When cost is used, cell removal is based on local conservation value divided by cell cost (efficiency), and now a high value for a cell can be explained with either (i) a very high occurrence level for some species or (ii) low cost for the cell. Thus, when cost information is used, the interpretation of a core-area becomes vague, and this should be recognized in planning. Therefore it is not recommended to use cost layers when trying to find out biologically most important areas with core-area Zonation.



This figure illustrates principles that core-area Zonation implements in numerical form. Essentially, the question is, if you have two (multiple) species, and you are going to lose a fraction (here one cell, marked as yellow) of one distribution, then where would you prefer to lose the cell from? (A) If you have two otherwise identical species, but one has a larger range remaining, then you prefer to lose from the species that has the larger range. (B) If you have two otherwise equal species, but one has relatively higher weight, then you prefer to lose from the distribution of the species with a lower weight. (C) You have two presently equal species with equally wide distributions. Then you prefer to lose from the species that has had a smaller historical reduction in the range (dashed line). (D) Within the distribution of a species, one prefers to lose from a location with a relatively low occurrence density (light gray).

2.3.2 Additive benefit function

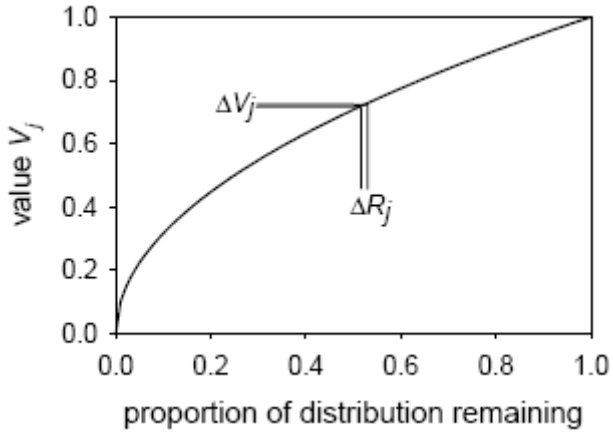
This section is mainly based on Moilanen (2007).

Compared to core-area Zonation, the additive benefit function takes into account all species proportions in a given cell instead of the one species that has the highest value. The program calculates first the loss of representation for each species as cell *i* is removed, and the δ_i -value of the cell is simply the sum over species-specific declines in value following the loss of cell *i*:

$$\delta_i = \sum_j \Delta V_j = \sum_j \left[V_j(R_j(S)) - V_j(R_j(S-i)) \right],$$

in which $R_j(S)$ is the representation of species j in remaining set of sites S, and (S-i) indicates the set of remaining cells minus cell *i*. Again the cell that has the smallest δ -value, will be removed.

© 2004-2006 Atte Moilanen



Above is a picture of a benefit function for species *j*. When a grid cell is removed from the landscape, the representation of each species occurring in the removed cell goes down by a small fraction ΔR_j and the respective value for that species goes down by ΔV_j. The total marginal loss in value is simply a sum over species-specific losses. Note that here the species has a standard weight of 1.0, but as with core-area Zonation it is possible to weight species differently when using additive benefit function. The effects of weighting are seen on the scale of the y-axis which will go from 0.0 to species weight w_i instead of going from 0.0 to 1.0.

Because the additive benefit function sums value over all species, the number of species in a cell has a higher significance compared to basic core-area Zonation. For example, using additive benefit function might lead to situation where species-poor cells are removed even though they have a high occurrence level for one or two rare species, because the δ_i -value of these cells is smaller than that for cells that have many common species with high representations. Thus, using the additive benefit function typically results in a reserve network that has a higher performance on average over all species, but which retains a lower minimum proportion of original distributions for the worst-off species compared to core-area Zonation (see figure of all three removal rules in section 2.3).

To find more information about the use of benefit functions, see:

Arponen, A., Heikkinen, R., Thomas, C.D. and A. Moilanen. 2005. The value of biodiversity in reserve selection: representation, species weighting and benefit functions. Conservation Biology 19: 2009-2014.

Arponen, A., Kondelin, H. and Moilanen, A. 2006. Area-based refinement for selection of reserve sites with the benefit-function approach. Conservation Biology, in press, corrected proofs available online - doi: 10.1111/j.1523-1739.2006.00607.x.

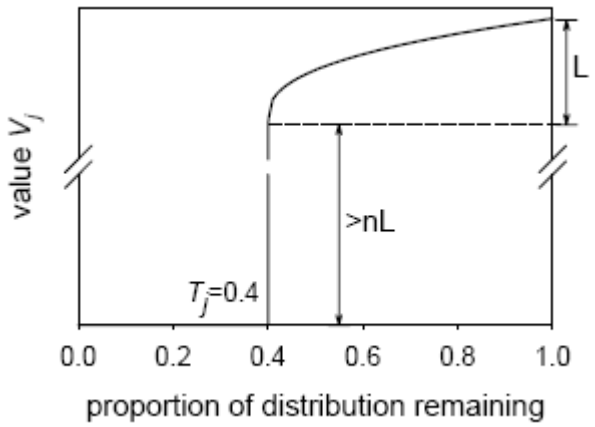
Cabeza, M. and A. Moilanen. 2006. Replacement cost: a useful measure of site value for conservation planning. Biological Conservation,132: 336-342.

2.3.3 Target-based planning

This section is mainly based on Moilanen (2007).

Target-based planning is implemented in Zonation by using a very particular type of a benefit function - the purpose of this special functional form is to enable the Zonation process to converge to a solution that is close to the proportional coverage minimum set solution for the data. In this function value V_j is zero until representation R_j reaches the target T_j. Then there is a step with the height of (n+1), where n is the number of species. When R_j increases above T_j and approaches 1, there is a convex increase in value, with a difference in value $[V_j(1)-V_j(T_j)]=1$. This means that the loss in value from dropping any one species below the target is higher than any summed loss over multiple species that stay above the target.

© 2004-2006 Atte Moilanen



The idea is that, as cells are iteratively removed, species representations will approach the species-specific targets from above, and that the convex formulation with increasing marginal losses will force species to approach targets in synchrony in terms of lost value. Thus, as one of the species approaches the target level, the program starts to avoid removing cells that contain that particular species (at the expense of other species) in order to retain the target. At some point it will not be possible to remove any more cells without violating the target for at least one species. After one of the species has declined below target, the remaining distribution of that species has no value for the reserve network. Thus removing cells where only this species occurs does not increase the loss of biological value from network anymore.

Note that when using target-based planning the species-specific weights have no function as the goal is to retain a given proportion of distributions for all of the species. However, it is possible to set different targets to different species. It is also recommended to avoid using very high warp factors to allow the program to find the most optimal solution near the targets.

2.3.4 General differences between cell removal rules

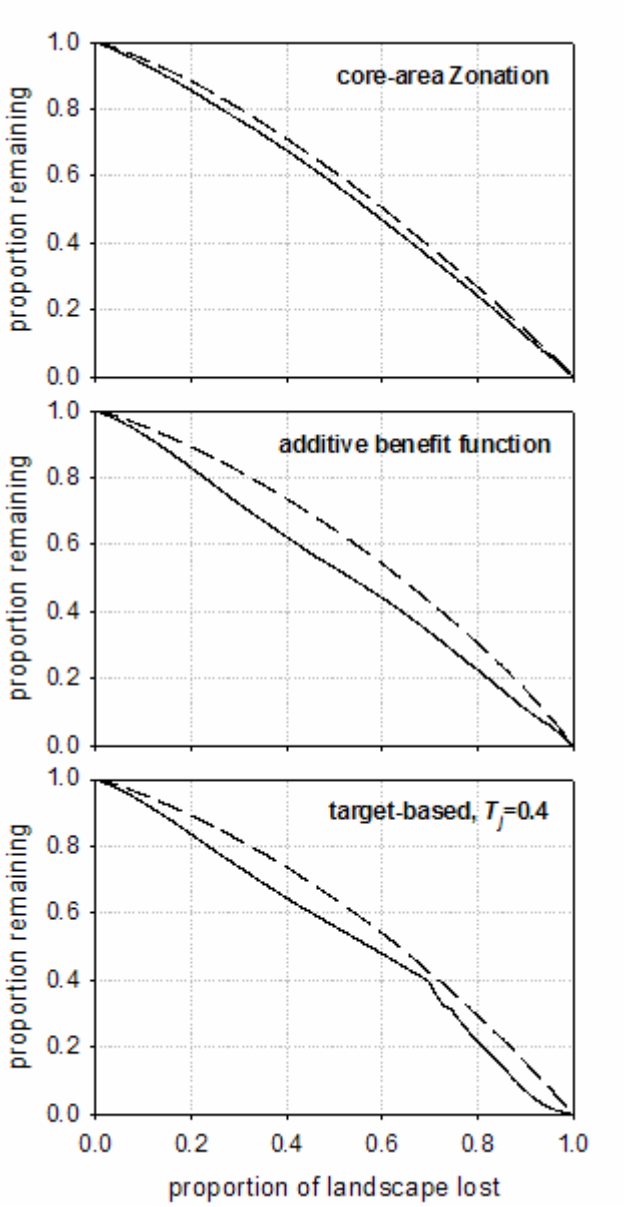
It is important to realize that there may be significant differences between different cell removal rule solutions and that the most preferable solution method depends on the goals of planning. Thus, different cell removal rules may be conceptually better suited for different situations.

- **Core-area Zonation** is most appropriate when there is a (i) definite set of species all of which are to be protected - tradeoffs between species are discouraged, (ii) the hierarchy of solutions and easy weighting of species is desired and (iii) importance is given to core-areas - locations with highest occurrence levels; occurrences in cells are not additive meaning that twenty locations with p=0.05 is not the same as one location with p=1.0.
- **The additive benefit function** formulation may be more appropriate when (i) the species are essentially surrogates or samples from a larger regional species pool, and tradeoffs between species are fully allowed, and (ii) the hierarchy of solutions and easy weighting of species is desired.
- **The targeting formulation** is most appropriate when (i) it is accurately known what proportion of the landscape can be had and the hierarchy is not needed, (ii) there is a definite set of species all of which are to be protected, (iii) occurrences are additive, and (iv) easy weighting of species is not needed. In target-based planning species weighting essentially needs to be done by giving species different targets.

The figure below (from Moilanen 2007) illustrates some general differences between the core-area Zonation, the additive benefit function formulation and the targeting benefit function. Here, the lines show how large proportion of species distributions is remaining in the landscape as cells are progressively removed. Overall, the additive benefit function has the highest average proportion over all species retained (dashed line), but it simultaneously has the smallest minimum proportion retained (solid line), because it favours species-rich areas over those areas that might be significant for the existence of one species, but that otherwise are species-poor. Core-area Zonation has a high minimum proportion combined with a relatively low average, because it retains the most

© 2004-2006 Atte Moilanen

significant areas of species (the "core areas") till the end, even thought these areas might be unsuitable for all the other species. The targeting benefit function does well in terms of finding the highest level of cell removal without having any species-specific targets violated. However, when further away from the target it does relatively poorly in terms of the minimum fraction over species retained. The problem with the targeting benefit function is that it is aimed at good performance at one particular set of targets, but the hierarchy of solutions is missing in the sense that good overall performance at other levels of cell removal, especially at a level where targets have been violated, cannot be guaranteed.



There are also differences between the cell removal rules on how much area they require for achieving a set conservation target. To get a given minimum fraction across species core-area Zonation requires more cells than the benefit function variants. This is because benefit function variants take occurrences as additive whereas core-area Zonation prefers the locations with very highest occurrence levels. However, if one investigates the number of cells needed to get the target distribution for an individual species, then core-area Zonation may require fewer cells because it prefers the higher-quality (density) cells. Thus, benefit function variants generate landscapes with many species occurring simultaneously at potentially low occurrence levels and with high overlap between species. Core-area Zonation produces solutions with species occurring at higher densities, but with less overlap between species.

© 2004-2006 Atte Moilanen

All these differences are such that they can logically be expected to occur in any data sets, with the magnitude of differences depending on the nestedness of species distributions. Differences would be largest when there are both (i) substantial regional differences in species richness and occurrence levels combined with (ii) a generally low overlap between species distributions. In this case core-area Zonation could catch cores of species occurring in species-poor areas whereas the additive benefit function would concentrate the solution more towards species-rich locations, where cells have high aggregate value over species.

Core-area Zonation and presence-absence data

Note that when using presence-absence data, all cells where a species is present receive an equal value (of 1). Thus, in P/A data there apparently are no core-areas of particular importance for the species, and it might seem pointless to use core-area Zonation as the cell removal rule. But this is not the case. First of all, if you use any additional analyses such as aggregation methods or the uncertainty analysis, the value of the cell will be calculated based on not only the species data, but other features as well (e.g. connectivity of the cell). Thus, differences between areas where the species is present do emerge. Secondly, even though in presence/absence data there are no core areas in terms of relatively higher occupancy densities, there still is the significant difference in the cell removal process between core-area Zonation and additive benefit functions. We highlight this with an example. Let us assume we have a landscape where 7 different species occur. Six of these species have overlapping distributions and one (denoted here as species A) has a distribution isolated from the other species. Because benefit functions take species occurrences as additive, the cells in sites where distributions of several species overlap receive a higher value than the cells where only one species occurs, as is the case with species A. Thus, in the cell removal process the additive benefit function would always favour cells with multiple species over the cells of species A, which would lead to unequal preservation of species (in other words species A would loose its distribution much more quickly than the other species). In contrast, Core-area Zonation would retain all species distributions equally, meaning that species A would loose its distribution at the same pace as do the other six species. This conclusion stays the same even when using presence-absence data.

2.4 Inducing reserve network aggregation

Fragmentation is an undesirable characteristic in reserve design as it has been concluded in many studies that species persist poorly in small and isolated patches. Also, implementing a fragmented reserve network may be awkward and expensive. In this section we introduce three different aggregation methods that can be used when running analyses with the Zonation program. These methods produce relatively more compact solutions. Note, however, that aggregation always involves trade-offs. There is usually an *apparent* biological cost in more aggregated solutions because in many cases it is necessary to include lower-quality habitats into the reserve network in order to increase connectivity. In reality this apparent loss is more than offset by benefits of having a well-connected area. Thus, it is recommended to use aggregation methods in reserve planning as the cost of loosing a minor amount biologically valuable areas is usually low compared to the benefits of high connectivity. For more information on true and apparent costs related to aggregation, see Moilanen and Wintle 2006 and 2007.

There are some distinct differences between the aggregation methods in Zonation, and choosing the right one depends on conservation targets and computational issues.

- **Boundary Length Penalty** (BPL) has been the most commonly used way to introduce aggregation to reserve planning. However, it is important to understand that BLP is a general, non-species-specific aggregation method which does not asses the actual effects of fragmentation on species. Rather the method only uses a penalty on a structural characteristic of the reserve network (boundary length) to produce more compact reserve network solution. The method is computationally quick and effective, but might not be biologically most realistic.

- **Distribution Smoothing** is a species-specific aggregation method which retains areas that are well connected to others, thus resulting a more compact solution. The connectivity of sites is determined with a smoothing kernel, which means that the value of a cell is "smoothed" to the surrounding area. Another way of looking at distribution

© 2004-2006 Atte Moilanen

smoothing is, that it does a two-dimensional habitat density calculation, identifying areas of high habitat quality and density. Consequently, cells that have many occupied cells around them receive a higher value than the isolated ones. The widths of the smoothing kernel are species-specific, implicitly expressing the species dispersal capability. This aggregation method is computationally very quick. However, it assumes that fragmentation (low connectivity) is generally bad for all species and it always favours uniform areas over patchy ones.

- **Boundary Quality Penalty** (BQP) is biologically the most realistic aggregation method included in Zonation. This method describes how the local value of a site for a species is influenced by the loss of surrounding habitat. The change in local value is based on species-specific responses to neighborhood habitat loss, thus local value may also increase if the site includes species that benefit from fragmentation. The downside of this method is the required computation time, which is much higher compared to the other two aggregation methods. This is because each cell removal influences the habitat value in all remaining neighbourhood cells, which needs to be accounted for in the cell removal process.

If you are including aggregation into your analysis, it is recommended not to use different aggregation methods simultaneously due to difficulties in interpreting results.

2.4.1 Distribution smoothing

This section is mainly based on Moilanen *et al.* 2005 - *Prioritising multiple-use landscapes for conservation: methods for large multi-species planning problems* (*Proc. R. Soc. B*, **272**, p. 1885-1891) and Moilanen and Wintle 2006 - *Uncertainty analysis favours selection of spatially aggregated reserve structures* (*Biol. Conserv.*, **129**, p. 427-434). Instructions to how to use distribution smoothing in Zonation can be found in section 3.5.2.

The first aggregation method described here is called distribution smoothing. When using distribution smoothing, planning is based on a connectivity surface computed from the original species distributions that have been input into zonation. The calculation that is applied to each species distribution is identical to the calculation of a metapopulation-dynamical connectivity measure, where the connectivity value is directly proportional to the number of migrants expected at that location in the landscape. Technically, the computation is a two-dimensional kernel smoothing using a species-specific parameter (width of the smoothing kernel).

For practical purposes, distribution smoothing identifies areas that have on average high occupancy levels for species. The smoothing very effectively identifies important semi-continuous regions where the species has overall high levels of occurrence, although not necessarily in every grid cell. In contrast, relatively scattered occurrences in fragmented habitat lose value. As the distribution of the species in the landscape becomes smoother, populations in fragmented areas end up with less value relative to continuous areas with the same average probability of occurrence.

Note that distribution smoothing should be used with care if the data includes a species that lives happily as a metapopulation in a fragmented habitat - smoothing should be narrow for this species at least if the habitat matrix is taken as partially suitable for the species. Distribution smoothing is a convenient technique to apply because it can be run as a relatively fast preprocessing step before going on to the zonation analysis itself. The appropriate level of smoothing for a given species would be determined based on a conception of the typical dispersal distances for that species, or from information concerning home range sizes for the species.

When using smoothing, the value for species *j* in a focal cell *i* is

$$O_{ij}' = \sum_x \sum_y \exp(-\alpha_j d(x-u, y-r)) O_{ij},$$

where O_{ij} is the original occurrence level of species *j* at cell *i*. Cell *i* is located in (*u*,*r*) and *d*(*x*-*u*, *y*-*r*) is the distance between locations (*x*,*y*) and (*u*,*r*). The summation is over the landscape grid and α_i is the parameter of the dispersal kernel for species *j*. This is a two-dimension kernel smoothing using a radially symmetric negative exponential (dispersal) kernel.

© 2004-2006 Atte Moilanen

2.4.2 Boundary Quality Penalty (BQP)

This section is mainly based on Moilanen and Wintle (2007).The boundary quality penalty - a quantitative method for approximating species responses to fragmentation in reserve selection. *Conservation Biology*, in press. Instructions to how to use BQP in Zonation can be found in section 3.5.3.

The boundary quality penalty is a quantitative species-specific way of inducing aggregation into Zonation solutions. It can be seen as a way of approximating nonlinear effects of connectivity that may be present in habitat models. The rationale behind the BQP goes as follows.

There are very many different statistical species distribution modelling techniques (a.k.a. habitat models, resource selection functions, ...). Typically, in such models the abundance of a species at a location is influenced not only by local habitat quality, but also by habitat in the neighbourhood of the location. Such a neighbourhood influence essentially states that the species is somehow dependent on connectivity or edge effects or both.

Now, ideally, reserve selection would be directly based on nonlinear habitat models with neighbourhood effects. However, this is not realistically possible, because it would make reserve selection computationally very, very slow. Also, implementing dozens of different habitat modelling techniques efficiently into reserve selection software would be an enormous task. Herein enters the BQP.

The BQP is a mechanism for approximating the aggregate response of a species to edge effects and metapopulation size and connectivity. It can be seen as a way of exploiting the connectivity response that is present for a species in a habitat model. Essentially, one uses the habitat model for two things. First, one predicts an abundance or probability of occurrence into every cell in the landscape – giving the standard input layer for one species. Additionally, one analyses the habitat model to find out what kind of an aggregate response to habitat loss and fragmentation does the species have. And this response is transferred into Zonation as a standardized curve, which mediates the boundary quality effect in Zonation.

Different species can have different responses to fragmentation and habitat loss, which are entered into Zonation as two BQP components: (i) a species-specific radius and (ii) a response curve. First, the radius. The effect of habitat loss can be localized (the species only has a narrow edge effect or so), or, the effects can extend over a longer distance, as could be the case with a timid larger animal that avoids human proximity – habitat loss could negatively influence such a species from a long distance away. By setting a species-specific radius, one can model how close habitat loss influences the species. Note that inside the radius only the loss of those cells that have data on the particular species (in other words cells that are not marked as missing data) can influence the value of the focal cell.

The second component, the response curve, specifies the kind of effect neighbourhood habitat loss has on the species. First, there could be an absence of effect, which would be modelled by a flat line (no effect). Then, the species could suffer variable degrees of loss in local population density if there is neighbourhood habitat loss. For example, you could have a relatively insensitive species, which loses half of the population density when the focal cell has lost all it neighbours from inside the species-specific buffer. Then again, the species could be very sensitive to neighbourhood fragmentation – all local value could be lost when only half of the neighbouring cells have been lost. And finally, a species could even favour fragmentation, which would be modelled by a response curve that goes above 1 at some levels of habitat loss.

© 2004-2006 Atte Moilanen

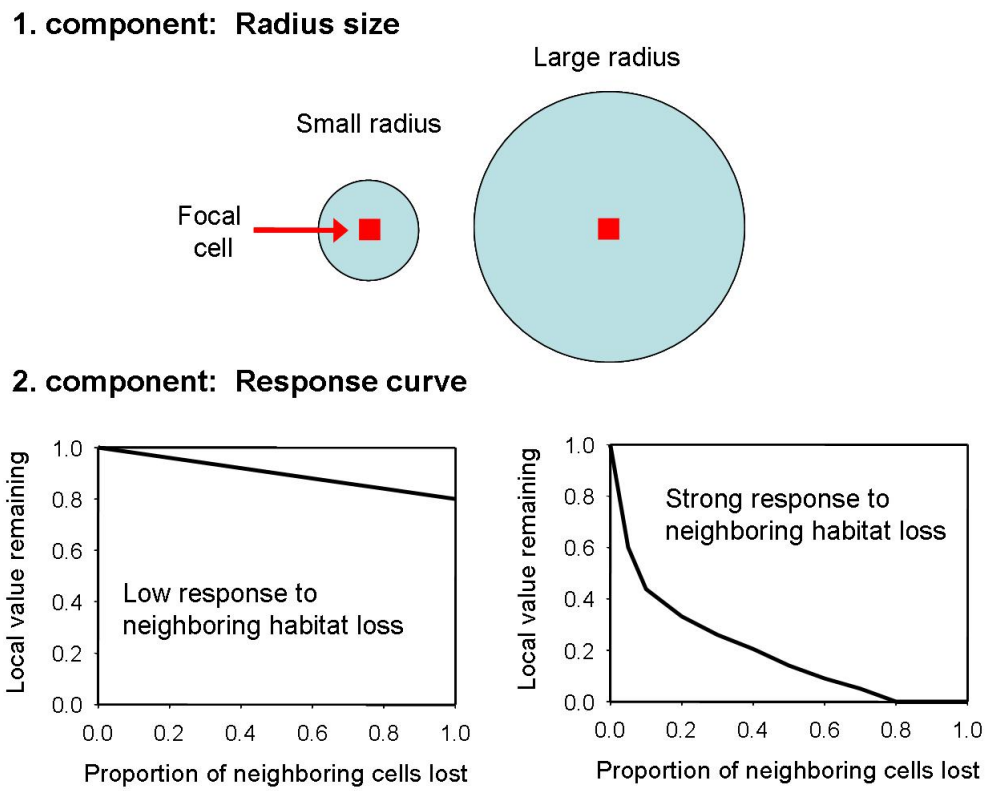


Figure clarifying the two components used when specifying the BQP for a species.

For the exact way of analysing a habitat model to get the species-specific response, see Moilanen and Wintle (2007). Note also that the BQP curves need not be derived from habitat models. One could also use expert opinion to guesstimate the response of the species to neighbourhood habitat loss. The hypothetical curve would then be entered into Zonation – it makes no difference for the Zonation process how the BQP-curves were obtained.

Note that there are major differences between distribution smoothing and the BQP even though both induce aggregation in a species-specific manner. First, from a practical point, the BQP is much slower to run as the effect of removing a cell is not only local but extends over the neighbourhood area which needs to be accounted for in computations. Second, the BQP is biologically better justified. The BQP definitions can be based directly on species responses in statistical habitat models. The difference between the methods would be most strikingly visible in fragmented areas. Distribution smoothing perceives the value of fragmented areas as relatively low. In comparison, the BQP could recognize a species that happily lives as a metapopulation in a fragmented environment – the response for that species would be such that it is recognized that the species can have high-value habitats in fragmented areas.

In the implementation of the BQP into Zonation, the value of a cell that is removed is now divided into two components (i) local value, which is as before, and (ii) loss of conservation value in the neighbourhood of the focal cell as modelled via the BQP specification. Thus with BQP the effect of cell removal is not only the loss of the value in the cell itself but also a (potentially species-specific) reduction in quality in the neighbourhood cells:

$$\delta_i = \max_j \frac{w_j}{c_i}\left\{ H_j\left(\frac{n_{ij}}{n^*_{ij}}\right)Q_{ij}(S) + \sum_{k \in N_j(i)} Q_{kj}(S)\left[H_j\left(\frac{n_{kj}}{n^*_{kj}}\right) - H_j\left(\frac{n_{kj}-1}{n^*_{kj}}\right)\right]\right\},$$

where $N_j(i)$ indicates the cells (containing data for that species) within the species-specific radius of cell i for species j. Denoting by h the fraction of original neighbours that have been lost from within the species-specific buffer around the site, $H_j(h)$ is the proportion of the original value of cell k

© 2004-2006 Atte Moilanen

remaining for species *j* when the focal cell has fraction *h* of its neighbours remaining. The fraction of cells remaining is simply $h = n_{kj} / n_{kj}^*$, where n_{kj} is the number of neighbours remaining for cell *k* within the buffer radius of species *j*, and n_{kj}^* is the original number of neighbours. The loss term in the curly brackets is divided into two, local loss and loss in the neighbourhood of the focal cell. Local loss is the fraction remaining of the original value of the focal cell *i* - if many of its neighbours have already been lost, the value of $Q_{ij}(S)$ has been reduced. Loss in the neighbourhood is mediated via the loss of one cell from the number of neighbours, which goes down from n_{ki} to n_{ki} - 1. (Note that the formula above is employed as it is only for the core-area Zonation. For additive benefit function and target-based planning the formula includes few trivial differences, but the concept behind BQP is the same in all cases.)

The size of the neighbourhood of a cell and the effects of habitat loss are defined separately for each species according to habitat models, which themselves mediate the boundary quality penalty. Because BQP ranks the cells based on the responses of species to fragmentation, also species that actually benefit from the loss of surrounding habitats will be equally protected (compare distribution smoothing).

2.4.3 Boundary Length Penalty (BLP)

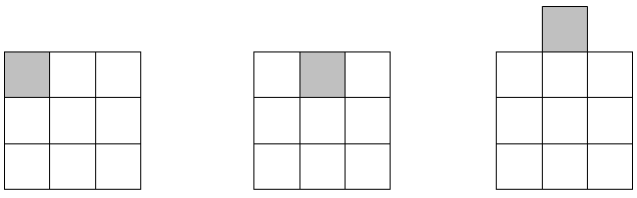
This section is mainly based on Moilanen and Wintle (2007).

The most common way of adding aggregation into a reserve network has been the boundary length penalty. This method is qualitative in the sense that the estimated conservation value of individual cells, or consequently the conservation value of the entire reserve network, is not influenced by the degree of fragmentation, but rather, aggregation is induced via a penalty given for the boundary length of the reserve.

When using the boundary length penalty, the hierarchy of cell removal is based on both species occurrence levels in cells and the increase/decrease of boundary length that results from the removal of a cell. The boundary length penalty can in the context of core-area Zonation be formulated as:

$$\delta_i = \max_j \frac{Q_{ij}(S) w_j}{c_i} + \beta \cdot \Delta(BL / A),$$

where $\Delta(BL/A)$ is the change in boundary length/area -ratio of the reserve network following removal of cell *i*, and β is a constant defining the strength of the boundary length penalty. If cell removal decreases boundary length, $\Delta(BL/A)$ receives a negative value and the value of δ_i for cell *i* decreases, indicating that it is relatively advantageous to remove the cell because removing it reduces fragmentation.



$\Delta L = 0$ $\Delta L = +2$ $\Delta L = -2$

Above is a picture showing how different cell removal options would influence the boundary length. The boundary length is calculated in the terms of cell edges. Removing the gray cell in the first example results in no changes in boundary length for as two edges are removed while another two are gained. In the second example the cell removal leads to the loss of one edge, but also to the gain of three new edges. Thus as a result the total change in boundary length is +2, and so on. To get from ΔL *to* $\Delta(BL/A)$ one needs to account for both the change in boundary length and the decrease of the reserve area by one.

Note that BLP is different from both distribution smoothing and the BQP. First, the BLP is not a species-specific way of handling reserve connectivity. It simply uses a penalty term that devalues

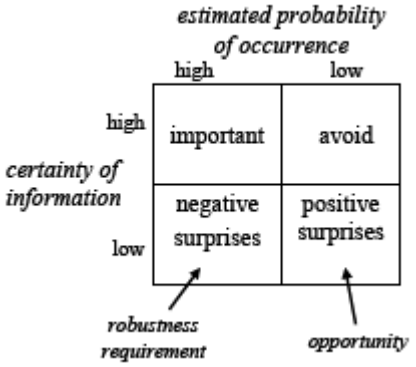
© 2004-2006 Atte Moilanen

reserve structures with lots of edge. This is completely qualitative; there is no species-specific parameter or response. Like distribution smoothing, the BLP may be expected to perform poorly for species that happily occur in fragmented habitats. This is because the BLP qualitatively favours structurally connected areas, and it will therefore have a tendency to remove small habitat fragments from the solution irrespective of whether some species can actually persist in them or not.

2.5 Uncertainty analysis

A common problem with conservation planning is uncertainty of planning inputs. Mostly these uncertainties are due to lack of data - we simply do not have a comprehensive database with accurate information of the distribution of every species. Uncertainty can also arise, for example, from outdated or false observations, the use of predicted data (e.g. distribution models), or from any future factors such as the potential for anthropogenic land-use changes, or climate change.

Taking into account both biological value and uncertainty creates a prospect of four scenarios. (1) Areas with high conservation value and high certainty of that information would be important for conservation. (2) Areas with low conservation value and high certainty (car parks, etc.) would ordinarily rank low among conservation priorities. (3) Areas with high estimated conservation value, but low certainty have potential for producing negative surprises for conservation. (4) Finally, areas with low conservation value and also low certainty have potential for producing positive surprises.



The goal of uncertainty analysis in reserve selection is to implement and evaluate trade-offs between biological quality and the certainty of that information. Ideally, one would identify a reserve network that guarantees high biological quality despite some uncertainty in input data. Uncertainty analysis could also be used for evaluating the opportunities arising from uncertainty, that is, potential for positive surprises.

Here we introduce two methods of uncertainty analysis that can be used in the Zonation context. The first method is called **distribution discounting**, which enables the ranking of the landscape using species distribution data that includes uncertainties. Our second method is for testing reserve network structures to see how robust they are against uncertain negative influences of habitat loss and fragmentation.

For more information about the aims and methods of uncertainty analyses in reserve selection, see:

Moilanen, A., Runge, M. C., Elith, J., Tyre, A., Carmel, Y., Fegraus, E., Wintle, B., Burgman, M. and Y. Ben-Haim. 2006. Planning for robust reserve networks using uncertainty analysis. Ecological Modelling 199: 115-124.

Moilanen, A. and Wintle, B.A. 2006. Uncertainty analysis favours selection of spatially aggregated reserve structures. Biological Conservation 129: 427-434.

Moilanen, A., Wintle, B.A., Elith, J. and Burgman, M. 2006. Uncertainty analysis for regional-scale reserve selection. Conservation Biology 20: 1688-1697

© 2004-2006 Atte Moilanen

2.5.1 Uncertainty in species distributions, distribution discounting

This section is mainly based on Moilanen *et al.* 2006. Uncertainty analysis for regional-scale reserve selection. *Conservation Biology* **20**: 1688-1697. Instructions for how to use distribution discounting in Zonation can be found in section 3.5.4.

Distribution discounting is a method for including uncertainty analysis into the conservation prioritization done in Zonation. This method helps you find the most robust solutions, those that most likely achieve a conservation goal given a level of uncertainty in species distributions. This analysis utilizes both the estimated biological value (probability of occurrence) of a species in a cell, and the certainty of that information.

Looking for robust reserve networks

In the framework of uncertainty analysis, one goal for reserve selection would be to find those network candidates that would achieve the given conservation targets despite uncertainty in input data. Thus, cells need to be ranked so that the highest priority is given to cells that have both relatively high conservation value and high certainty of information. In Zonation, uncertainty analysis has been implemented according to a convenient formulation that uses information-gap decision theory (see Ben-Haim 2006).

Conceptually, relevant components of the info-gap theory are

1. The *nominal model*. This is your best set of predictions for species.
2. The *uncertainty model*. This states that even though you do have a nominal estimate, your true probabilities of occurrence are certain to deviate from your nominal model. The uncertainty model specifies a set of bounds that expand around the nominal estimate as a function of an uncertainty parameter, α.
3. A *performance function*. This is a function measuring how well you are doing, for example, what is the proportion of species distributions that would be covered by a given set of areas.
4. *Robustness function*. This function measures "how large can the horizon of uncertainty α be so that conservation goals are still met even if you take the most adverse choice of probabilities from inside the uncertainty bounds". A good reserve candidate is such that it achieves goals while allowing for high uncertainty (α). The *robust optimal reserve candidate* is the one that achieves conservation goals while allowing for highest uncertainty.

Ben-Haim, Y. 2006. *Info-gap decision theory: Decisions under severe uncertainty*, 2nd edition. Elsevier Academic Press.

In more detail: The occurrence of species *s* in a cell *c* (here indicated as p^*_{sc}) is by no means certain, but merely the nominal "best guess" probability. Thus the true probability $p_{sc} \in [0,1]$ could be within an interval given by:

$$\left(p^*_{sc} - \alpha w_{sc}\right) \le p_{sc} \le \left(p^*_{sc} + \alpha w_{sc}\right) \qquad (1)$$

where α is the horizon of uncertainty and w_{sc} is any error measure related to the accuracy of p^*_{sc} (for species *s* in cell *c*). Thus the true probability p_{sc} could be either higher or lower than the estimate p^*_{sc}, with bounds for p_{sc} determined by α and the relative error measure w_{sc}, which could be, for example, related to the accuracy of statistical prediction. The model of Eq. (1) is called an uniform bound model in info-gap terminology.

When using predictions based on logistic regression habitat models, a plausible model for uncertainty is to define the uncertainty interval in logit space, where w_{sc} is the standard error for the linear predictor of a logistic regression:

$$\left|\mathrm{logit}\left(p_{sc}\right) - \mathrm{logit}\left(p^*_{sc}\right)\right| < \alpha w_{sc} \qquad (2)$$

© 2004-2006 Atte Moilanen

According to info-gap theory, one should favour reserve structures that achieve given conservation targets even with the most adverse choice of probabilities (in other words, in the worst case scenario). Given the present definitions, the most adverse choice of probabilities occurs when all probabilities are at their lower bounds (this is when the lowest expected number of populations is obtained):

$$\text{logit}(p_{sc}) = \text{logit}(p^*_{sc}) - \alpha w_{sc} \qquad (3)$$

Thus the program calculates the discounted biological value of a cell by reducing (discounting) the value of the logit of probability (p^*_{sc}) by a multiple of the error (αw_{sc}). In the distribution discounting technique, the original estimated occurrence data is simply replaced by the discounted data before proceeding to do the Zonation run. Thus, one Zonation run with discounted data is needed for each value of the horizon of uncertainty, α.

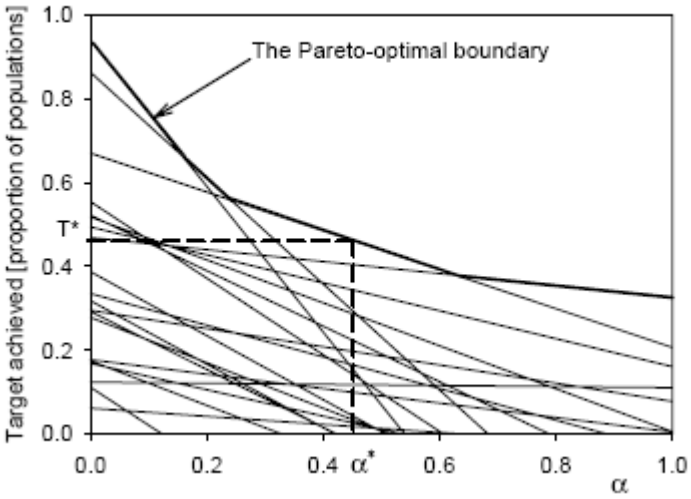
But how to determine the horizon of uncertainty, α? As mentioned above, the relative error w_{sc} can be any error measure related to the predicted species distribution. It can, for example, be a statistical error (e.g. the length of the lower half of the 95% confidence interval) or a probability of future anthropogenic threat, or both. The value of α, on the other hand, is unknown and has no correct value. The way forward is to investigate how different reserve network candidates perform under increasing uncertainty. In practise, the way is to try out several levels of α to see what areas are selected. If an area is always selected irrespective of the value of α, then the area is important for sure. If the area is selected with low α but not with high alpha, then the area is selected because of the occurrence of an uncertain biological feature. If the area is not selected with low α but is selected with high alpha, then something of interest occurs in the area with relatively low density but high certainty. Based on such uncertainty analysis, one can split the landscape in three categories of areas: (i) areas that are good for sure, (ii) areas that are never selected and thus have low priority and (iii) areas that are selected with some levels of uncertainty - these areas may need further investigation before a choice of conservation priority for them can be fixed.

Distribution discounting uses the following algorithm for finding robust-optimal reserve designs:

1. Specify robustness requirement α.
2. *Distribution discounting.* Read in species information. For every species and cell, apply Eq. (3) or its analogue, depending on type of data/uncertainty model.
3. Use any reserve selection algorithm (here Zonation) to search over spatial patterns. The robust optimal design **X*** (at the given level of α) is the one achieving the highest possible conservation value.

The advantage of this approach is that the worst-case probability set (Eq. 3) has to be calculated only once (item 2.), and thereafter the contributions of cell to representation levels, p_{sc}, do not change in the reserve selection process. Testing several α-values allows you to outline how different reserve structures behave in increasing uncertainty. Some designs are always bad, some are good according to nominal habitat model predictions, but bad if uncertainty is incorporated into the models. Others have intermediate nominal performance, but have a good robustness to uncertainty. The robust-optimal designs are always at the **Pareto-optimal boundary** with respect to the target, as demonstrated below:

© 2004-2006 Atte Moilanen



Here each thin line represents one solution (spatial reserve structure). An increasing robustness requirement (α) implies that a decreasing biological value can be achieved reliably. The thick line is the Pareto-optimal boundary representing solutions that are optimal in the sense that increased biological value can only be obtained with the cost of lowered robustness, and *vice versa*. When doing reserve selection on a large grid, there is a huge number of potential reserve structures, but only one or few of them would correspond to the Pareto-optimal boundary at any given α-level and resource (fraction of landscape). Any solution not at the Pareto-optimal boundary is inferior in the sense that another solution exists with either higher biological value or higher robustness or both. The distribution discounting technique used inside Zonation automatically identifies the robust-optimal nested Zonation set of solutions for the given level of α.

2.5.2 Uncertainty in the effects of landscape fragmentation

This section is mainly based on Moilanen & Wintle (2006). Uncertainty analysis favours selection of spatially aggregated reserve structures. *Biological Conservation* **129**: 427-434. Instructions of how to use fragmentation uncertainty analysis in Zonation can be found in section 3.6.4. This analysis is for investigating how robust a given reserve network is to potential negative effects of fragmentation. This is a minor analysis that would not be relevant for most applications of Zonation - essentially, it is intended for the investigation of the robustness of a network that has been designed without any spatial aggregation method. The description below is a brief description of the analysis, please see the original publication for details.

We start from the assumption that cells ending near the edge of a reserve network will end up with decreased conservation value due to negative edge effects, disturbance and disrupted spatial (meta)population dynamics. Just like distribution discounting, fragmentation uncertainty analysis is based on the info-gap theory. Since the main interest of this analysis is uncertainty in conservation value due to habitat loss and fragmentation, error rates (see section 2.5.1) are explicitly related to the amount of habitat loss occurring near the focal cell, assuming the habitat close to the reserve network border is degraded.

The error model chosen for this study specifies that the "true" value of a cell is inside an uncertainty interval;

$$f(\alpha L_c)p^*_{sc} \le p_{sc} \le \frac{p^*_{sc}}{f(\alpha L_c)} \qquad p_{sc} \in [0,1] \qquad (1)$$

where the relative error measure w_{sc} has been replaced by the proportion of cells lost from the neighbourhood of focal cell c, L_c. (This is the proportion of cells that were available but were not chosen into the reserve network.) The uncertainty model above is a proportional error model in the info-gap terminology (Ben-Haim, 2006). In the equation, $f(\alpha L_c)$ could be any decreasing function of L_c with $f(0)=1$, and $f(x) \in (0,1)$ for all $x \ge 0$. The condition $f(0)=1$ specifies that if nothing has been lost from the neighborhood of a cell, then the nominal predictions should be used as there is no

© 2004-2006 Atte Moilanen

uncertainty caused by nearby habitat loss. In the Zonation program a simple relationship $f(\alpha L_c)=\exp(-\alpha L_c)$ is used, but any other decreasing function would give similar results. With this relationship, if $\alpha=0$ (no uncertainty) or if there is no habitat loss ($L_c=0$), then *f*rom (1) it follows that $p_{sc}=p^*_{sc}$. Increasing the uncertainty parameter α or the fraction of habitat lost will result in a potential loss of conservation value in the target cell.

Note that it is not claimed that any correct value of α is known. Rather, the uncertainty analysis will proceed to analyse how robust different solutions (reserve network candidates) are to increasing uncertainty. The second component needed for the uncertainty analysis is a measure of the performance of a candidate reserve network as uncertainty is increased. The performance of species *s* in candidate reserve network **X**, $V_s(\mathbf{X},\mathbf{p})$, was defined as the proportion of the original full distribution of the species remaining in the given reserve structure **X**;

$$V_s(\mathbf{X},\mathbf{p})=\frac{\sum_c x_c p_{sc}}{\sum_c p^*_{sc}} \qquad (2)$$

where p^*_{sc} is the original value for species *s* in the cell *c*, and p_{sc} is the final value after the loss of neighbourhood habitat has been taken into account. x_c receives values depending whether the cell in question is included to the candidate reserve network ($x_c=1$) or not ($x_c=0$). Just like in distribution discounting, also here the evaluation of robustness means that we are interested in the most adverse choices. Therefore, we look at the lower bounds of probabilities. This means that in Eq. (2) p_{sc} is equal to $f(\alpha L_c)p^*_{sc}$.

Different reserve structures will be differentially resistant to negative effects of fragmentation - very fragmented reserve networks will have the characteristic that if species occurring in the network are sensitive to fragmentation, then the true value of the network can be much less than what is estimated based on an analysis that does not include explicit spatial effects. In contrast, a large and well-connected reserve will be relatively insensitive to negative effects of fragmentation, because only a small fraction of the reserve area will be close to the reserve edge. Essentially, such a reserve would have a large core. When running the fragmentation uncertainty analysis, the program calculates how much biological value might be lost from a candidate reserve network as the uncertainty and/or the fragmentation of surrounding habitats increases (see section 3.6.4).

2.6 Replacement cost analysis

This section is mainly based on Cabeza and Moilanen2006 (*Biological Conservation* **132**: 336-342).

Very seldom can reserve planning be started from a fresh table with areas that have no older reserves nor any restrictions for conservation (such as areas ear-marked for residential building). More commonly reserve networks are planned so, that due to logistic or social constraints, certain sites need to be included to, or excluded from the final solution. In most cases this leads to a suboptimal network either in terms of conservation value or in terms of the cost of achieving a given conservation goal. Instructions how to inlcude or exclude areas to a Zonation solution can be found in section 3.5.5 Inclusion/Exclusion cost analysis using mask files.

It is useful to be able to asses the degree of suboptimality of solutions compared to the optimal ones. Here we introduce a method called *replacement cost analysis,* which can be used to evaluate the effects of forced site inclusion/exclusion. *Replacement cost* refers to the **loss in solution value** given that the optimal cost-efficient solution cannot be had and that alternative solutions, with particular sites forcibly included or excluded, must be accepted. It tells us at what cost (biological or economic) can we exclude (or include) a site from the reserve network. Assuming a constant budget, the *exclusion cost* of that site is the loss in the network's conservation value that follows when a site that belongs to the optimal solution cannot be taken. The *inclusion cost* of a site is the loss in conservation value that must be accepted if a suboptimal site is forced into the reserve network. On the other hand, when the conservation budget is not fixed, replacement cost can also be defined in terms of the extra funding required to maintain conservation value that is equal to the value of the optimal solution. Thus, one can define four variants of replacement cost:

© 2004-2006 Atte Moilanen

1. *Biological exclusion cost.* Decrease in conservation value following forcible exclusion of a given (group of) site(s).

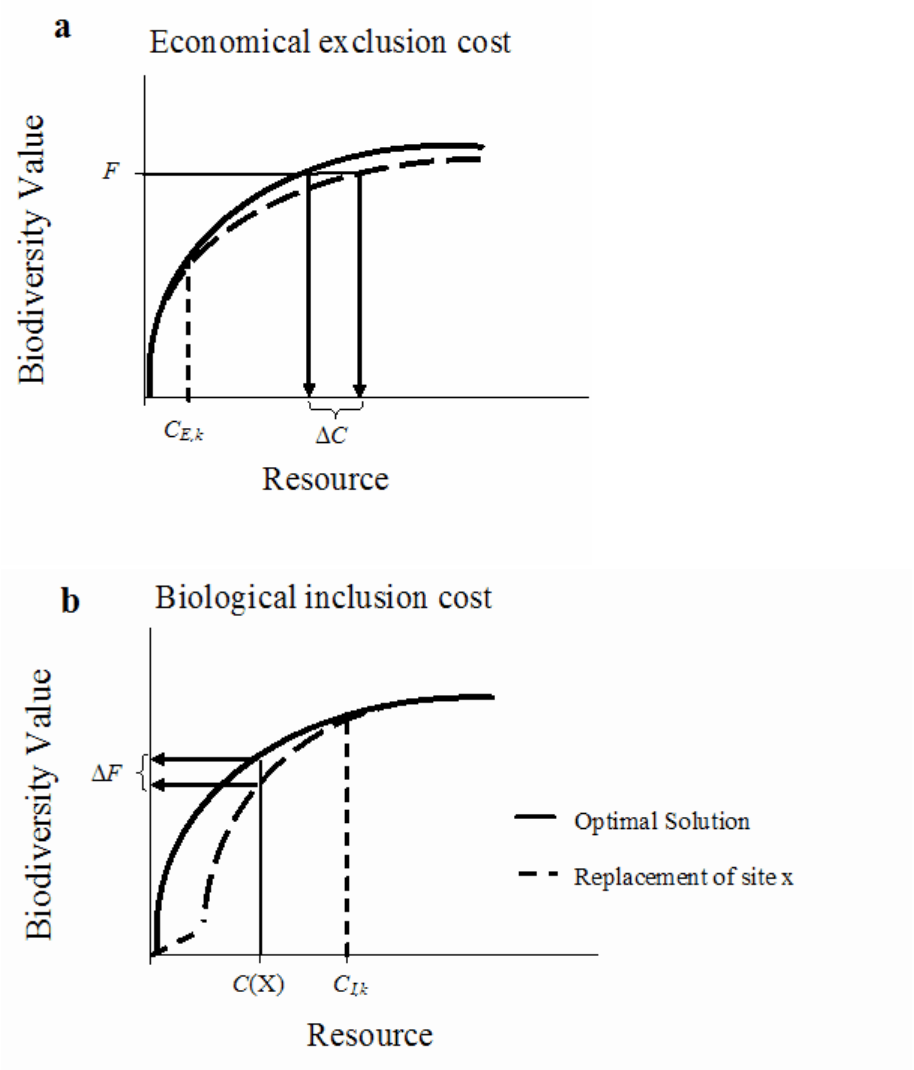
2. *Biological inclusion cost.* Decrease in conservation value following forcible (suboptimal) inclusion of a given (group of) site(s).

3. *Economic exclusion cost.* Increase in solution cost required to keep the same total conservation value following the forcible exclusion of a given (group of) site(s).

4. *Economic inclusion cost.* Increase in solution cost required to maintain conservation value following the forcible inclusion of a given (group of) site(s).

For practical purposes, the replacement cost is calculated in the following manner. First, find optimal reserve selection **X*** which has highest possible value $F(\mathbf{X}^*)$ obtainable with the available resource (C_{max}). Then rerun the analysis with some areas forced in or out. Replacement cost is the difference between the value of the optimal solution and the value of the new solution. We emphasize that **this does not mean keeping the optimal set of sites plus/minus a particular site**, **but finding a completely new solution given that the particular site(s) are forcibly included/excluded.**

A replacement cost of zero tells us that there exists an alternative solution with the same value as the current (best) solution has, i.e. same cost, and same conservation value (although obtained via a different selection of areas compared to the original optimal selection). A replacement cost larger than zero means that any alternative solution including/excluding the focal site(s) will have either a lower conservation value or a higher economic cost than the optimal one.



© 2004-2006 Atte Moilanen

A conceptual illustration of the *replacement cost* of a hypothetical site (a) in terms of increase in resources required to maintain value (ΔC) and (b) in terms of loss of biodiversity value (ΔF) (from Cabeza and Moilanen 2006). (a) *Exclusion cost*: the dashed line indicates the value of the best solution when site *x* is forcibly excluded. Up to a certain resource level, $C_{E.k}$, site *x* does not belong to the optimal solution and thus exclusion cost is zero. Even with $C > C_{E,k}$, exclusion cost can be zero if the site is fully exchangeable with another site or a combination of other sites. (b) *Inclusion cost*: the dashed line indicates the value of the best solution when a site is forced to be included in the solution. Inclusion cost is likely to be highest with low resource, when the forced inclusion of the unwanted site prevents the acquisition of other biologically much more valuable locations. At $C > C_{I,k}$, the focal site becomes included in the optimal set and inclusion cost becomes zero. (Note that the resource here should be understood the proportion of landscape retained in the Zonation.)

The figure also shows an example of how exclusion and inclusion can be expected to behave qualitatively. With a small resource ($< C_{E.k}$), the exclusion cost (a) of a site is likely to be zero, because the site would not be in the optimal set in any case. At a level $C_{E.k}$ the site becomes part of the optimal solution. With a resource slightly higher than $C_{E,k}$, it is likely that the exclusion of the site can be compensated with small cost, at least if there are many selection units. However, when the available resource is large, sites of less importance are included in the solution and the exclusion of a high-quality focal site has a clearly positive cost.

Inclusion cost (b) behaves differently. When a site that would not belong to the optimal solution is included in the network it generates an increase of cost even when the resource available is small because the resource is spent on suboptimal areas. With increasing resource availability, the inclusion cost gradually decreases. At a level $C_{I.k}$, the site would already become part of the optimal solution and inclusion cost thus becomes zero.

© 2004-2006 Atte Moilanen

2.7 Assumptions & limitations

This section lists some known assumptions and main limitations of the presently available zonation implementation.

- The Zonation software presently only accepts data in grids, in particular, it does not accept vector-based planning units or multi-cell planning units. This limitation is not conceptual and it may be removed in the future.

- Zonation is presently for doing an implement-in-one-go reserve/conservation plan. In particular, it does not include any explicit mechanism for handling multi-year planning with considerations of stochastic site availability and the possibility of site loss. Speculatively, it may be possible that suitably defined input layers or a clever use of cost files could be used for doing an analysis where approximate effects of habitat loss could be accounted for. This limitation most likely can be removed at least partially.

- At present Zonation only has a single option per selection unit, that is, protect or not, restore or not, maintain or not and so on. In a more advanced analysis one could envision multiple alternative outcomes for each location (e.g., different levels of protection or restoration). The currently available Zonation version does not allow for multiple alternative land-uses.

- At present, Zonation operates on input distributions of biodiversity elements (species, land cover types etc.). It does not operate on environmental surrogate information. This is not a conceptual limitation and it potentially could be lifted in a later version of Zonation.

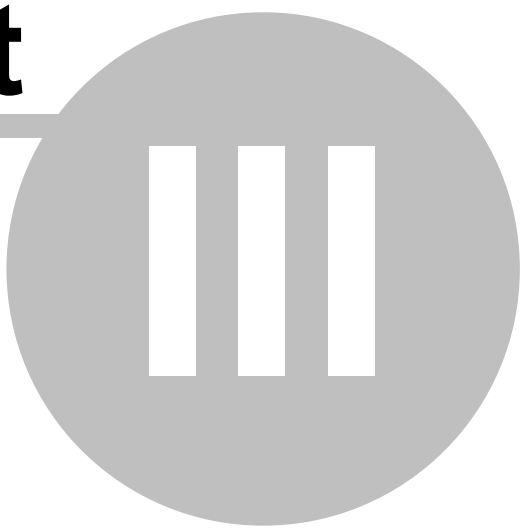
- The connectivity measures used in Zonation (in distribution smoothing and BQP) are simplistic in the sense that they are based on species-specific dispersal distances (or scales of landscape use), and influences of habitat loss. However, they do not include any explicit analyses of movement paths, such as least-cost path –type analyses.

- The Zonation software does not include a full GIS interface and only a limited set of analyses and graphs can be produced with the software. The analysis output files can however be imported into GIS software for further processing.

- The present software can use at maximum 4GB of memory on a PC, which sets the ultimate limit of how many species and in how large landscapes can be handled. This limitation is likely to be lifted in a forthcoming release of the software.

© 2004-2006 Atte Moilanen

Part



3 ZIG - The Zonation software

3.1 Introduction

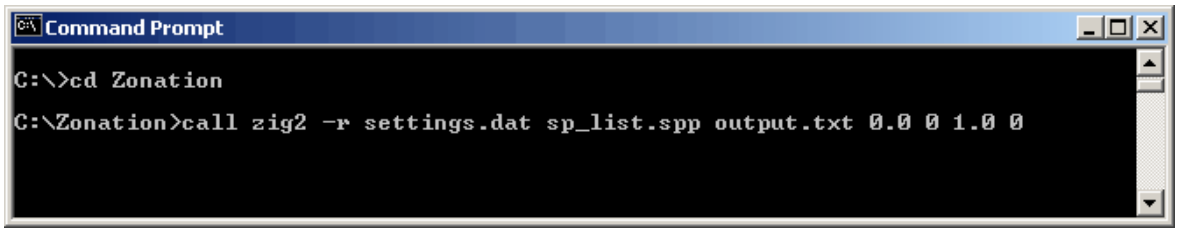
In the following sections we describe how the Zonation software is used, what kind input files it requires, what kind of output it produces and which are the analyses that can be done with the program. If a phrase is underlined in the text, it means that it is just mentioned here and explained in more detail in another section. Just click the word (if reading the manual pdf) or use the index to find these sections. For concepts and analyses implemented the software, see section 2.

3.2 Running Zonation

When running the Zonation program you have three options: You can operate the program by using either the Command prompt, the Windows interface or batch files. The Windows interface can be more easily approachable when familiarizing oneself with the program, but when running several more advanced analyses it is highly recommended to operate the program from command prompt together with batch files. These options are explained in the following sections.

Note that with Zonation you can also either (i) make new analyses or (ii) load old solutions. The solution loading option can be used either to review old solutions or to investigate how old solutions would perform under new assumptions (cross-compare).

3.2.1 Command prompt



Picture of basic Zonation call, when running a new solution without uncertainty analysis or distribution smoothing.

The Zonation can be run from the command prompt, from the directory in which **zig2.exe** and input files are located. To do this you need to

1. Open the command prompt from your "Start" -menu.
2. Use "`cd directory_name`" to change to the correct working directory which contains the zig2.exe and all the input and settings files.
3. Call the program with "`zig2`" followed by:
   - -r, if a new solution will be calculated, or -lfilename if an existing solution is loaded (the name of the rank.asc -file, e.g., `-loutput.rank.asc`)
   - Name of the Run settings file
   - Name of the Species list file
   - A name for the output files (`name.txt`). Remember to write the correct suffix after each file name.
   - Value of the uncertainty parameter α for the uncertainty analysis (UCA). If uncertainty is not included in the computation, this should be set to zero.
   - Value to determine whether distribution smoothing is used in the analysis (parameter = 1) or not (parameter = 0).

© 2004-2006 Atte Moilanen

- Factor for multiplying species-specific widths of the dispersal kernel (α -values, the second column in you species list file). This parameter helps you to produce multiple solutions with different dispersal kernel sizes without needing to change the kernel widths manually after each run. All kernel widths will be multiplied with this factor. To run more complicated solution groups (e.g. with several different factors varying), see section 3.2.4 for batch-run capability.
- Zero or one indicating whether the program window will be left open: 0 will leave the window open, and 1 will close the window allowing the program to move on to the next run. If a batch file is written for performing multiple runs, it is important to write 1 at the end of each line or the program will not proceed to the next Zonation run.

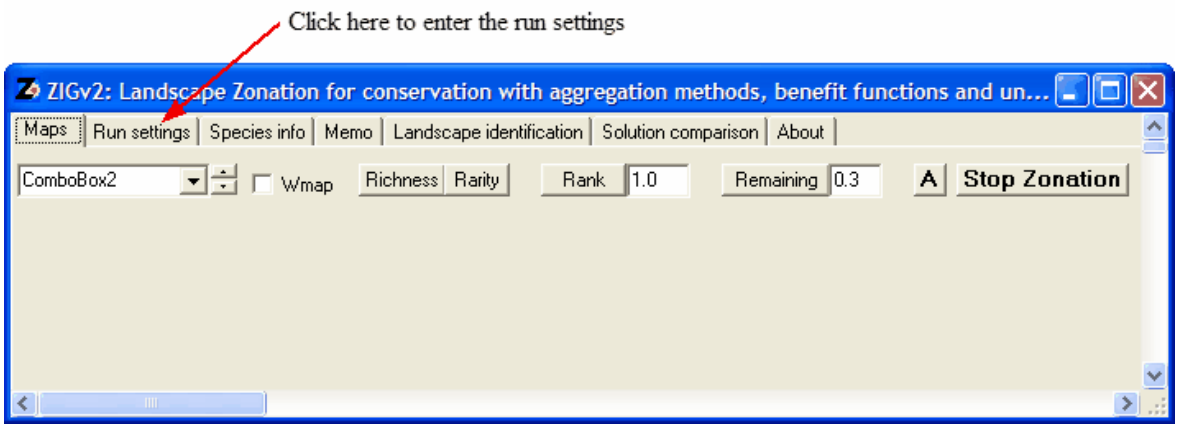
4. Press enter to initiate the computation.

Note that it is good to familiarize oneself with the command prompt and its functions, but to use the program efficiently it is much more practical to use batch files instead of rewriting the commands for each run (see section 3.2.4). In this example no aggregation has been included in the analysis. However, it is recommended that some aggregation methods (e.g. distribution smoothing, BQP etc.) would be used when running the final analysis to increase the true conservation value of the reserve network.

See also section 3.7 for basic commands that are useful when using the command prompt.

3.2.2 Windows interface

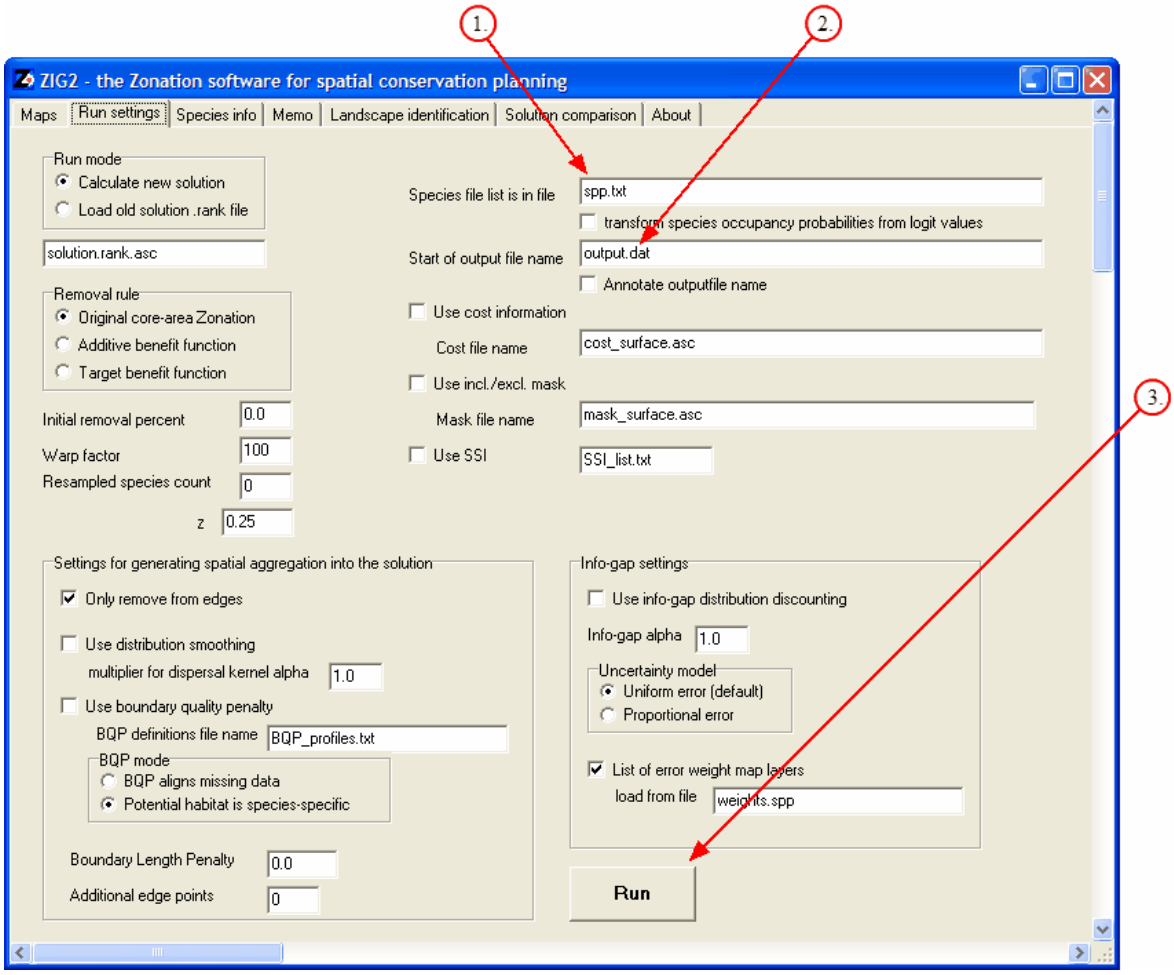
The program can also be operated by using the windows interface. Double clicking on the **zig2.exe** icon starts the windows version of the program. To run the program, go to the **Run settings - window.**



Picture of the Zonation interface when opened.

1. Enter the name of your species list file and
2. Give a suitable name for your output files. Remember to write the correct suffix after each file name (e.g. ouputfile**.txt**).
3. If needed, adjust the settings (see section 4.2.1, Run settings) and press the "Run" -button to initiate the computation.

© 2004-2006 Atte Moilanen



Picture of Run settings -window.

After running the program the results of your data are displayed in the **Maps -window**. Rest of the visual output is shown in the **Species info -window**. Note that although no aggregation has been included in this example, it is recommended that some aggregation methods (e.g. distribution smoothing, BQP etc.) would be used when running the final analysis to increase the conservation values of the solution.

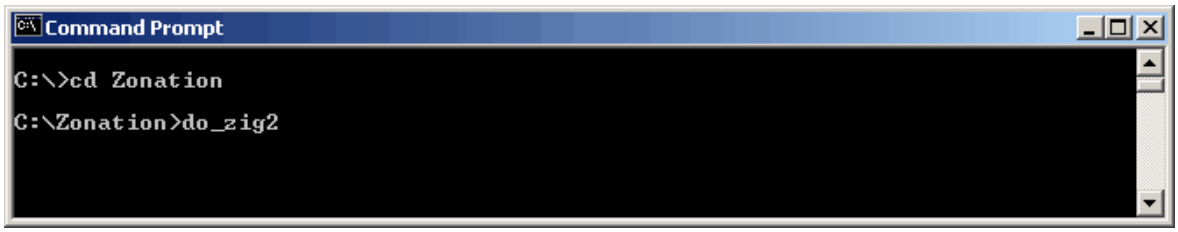
3.2.3 Batch-run capability

Your third possibility is to run the program with batch files. A batch file is a simple Windows/DOS command line file that can be used to give commands to Windows. Batch files can be created for example with notepad. This is done by writing the program call (same as when using the command prompt) on a new notepad document and saving it with the **batch file -extension** (.bat). The file name extension of a batch file has to be **.bat**. If there is anything else after the .bat -suffix, Windows can not identify the file as a command file. It is much more practical to use batch files instead of writing the commands in the command prompt for each run. There are several reasons:

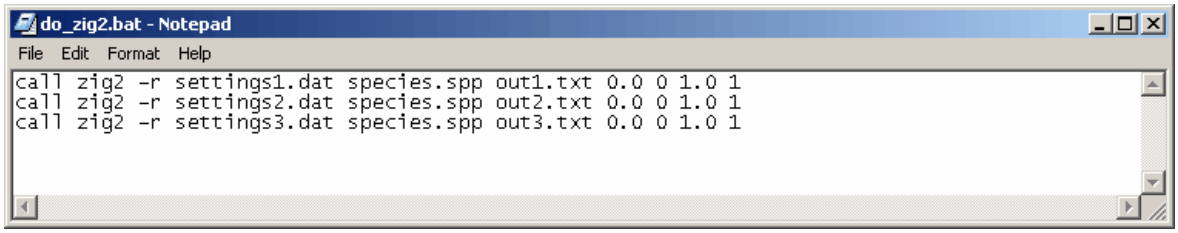
- You will save time.
- The information of your analysis (which input files and settings has been used) will be saved in the batch file and you can review them later.
- With batch files you can run multiple analyses without needing to adjust the setting between the runs.

A batch file is run simply by either double clicking the file icon or writing the name of the batch file in the command line in the command prompt and hitting enter (picture below). You can edit batch files with notepad or with the command prompt edit utility.

© 2004-2006 Atte Moilanen



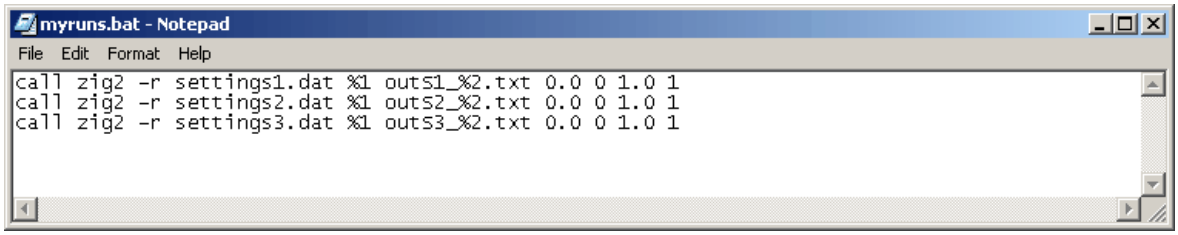
A batch file is useful, for example, if you want to experiment with different levels of distribution smoothing, uncertainty analysis, BQP etc. (several settings files) or with alternative species weighting schemes (several species list files). You can also use batch files to run the most complicated analyses (requiring long computation times) overnight or over the weekend. When you wish to run multiple analyses, the simplest batch file consists of several command lines, each calling the program with different parameters, e.g.


do_zig2.bat - Notepad
File Edit Format Help
call zig2 -r settings1.dat species.spp out1.txt 0.0 0 1.0 1
call zig2 -r settings2.dat species.spp out2.txt 0.0 0 1.0 1
call zig2 -r settings3.dat species.spp out3.txt 0.0 0 1.0 1

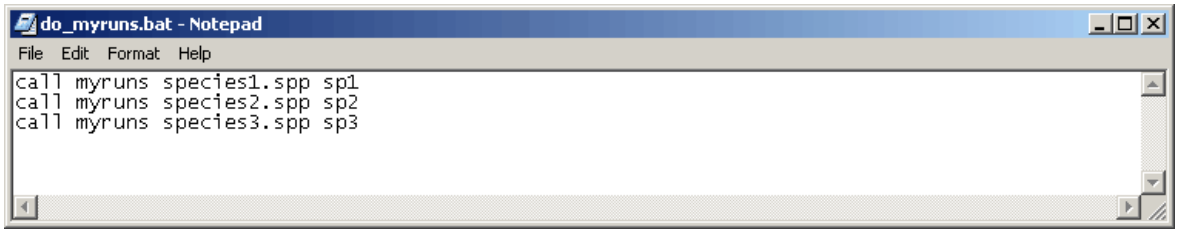
Here, the same species list file is run with three different settings. **Remember to identify the output files separately (give different names), or the program will overwrite old results after each run**.

Notice, however, that when performing multiple runs, you will have only the results that are automatically saved (see file output) and you will not be able to explore the results in any more detail with the windows interface. Further, you will not be able to perform the landscape identification procedure for each run, but will have to do that separately after using solution loading. This is because after each run the program will have to close in order to proceed to the next analysis run. Therefore there also has to be a 1 in the end of each row to close the program. If this parameter is 0, the program will not close itself and can not move to the next run.

The description so far cover the basic use of batch files, but another more complicated example follows below. If you want to alter more than one parameter simultaneously, then one way forward is to use multiple nested batch files. For instance, you might want to run the above batch (do_zig2.bat) with different species weights defined in separate species list files. To do this we first create a new file called "myruns.bat" and then adjust the settings from our example above:


myruns.bat - Notepad
File Edit Format Help
call zig2 -r settings1.dat %1 outS1_%2.txt 0.0 0 1.0 1
call zig2 -r settings2.dat %1 outS2_%2.txt 0.0 0 1.0 1
call zig2 -r settings3.dat %1 outS3_%2.txt 0.0 0 1.0 1

Then we create another batch file, which in turn calls the "my runs"-batch.

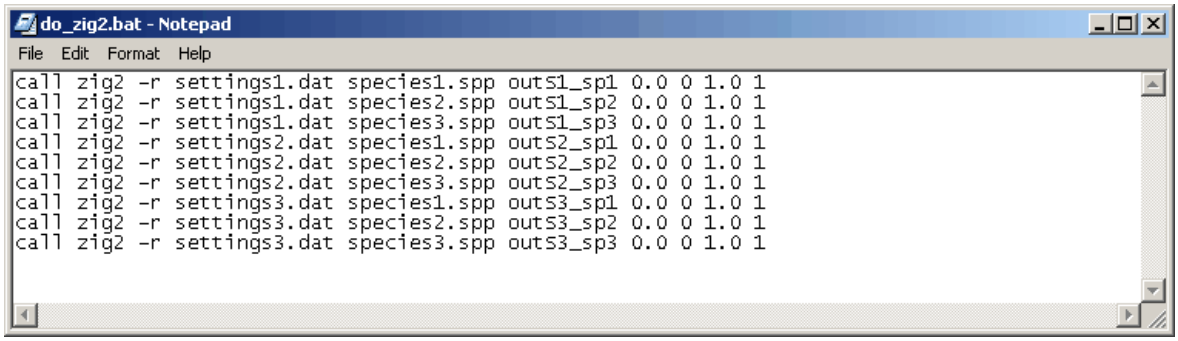


Here the first parameter after "my runs" defines which species list file is used when running the "my

© 2004-2006 Atte Moilanen

runs"-batch and the second parameter (sp1, sp2, sp3) defines a part of the output file name to distinguish which species file has been used in each run. In "my runs"-batch file these parameters will be referred as %1 and %2. When running the "do_my runs"-batch the program first calculates solutions using "species1.spp"-file with three different settings and giving each of the output files an ending "sp1" (outS1_sp1, outS2_sp1 and outS3_sp1). Then the program repeats the procedure with the other two species list files, "species2.spp" and "species3.spp". Thus, running the batch produces nine solutions with different settings and species weights composition.

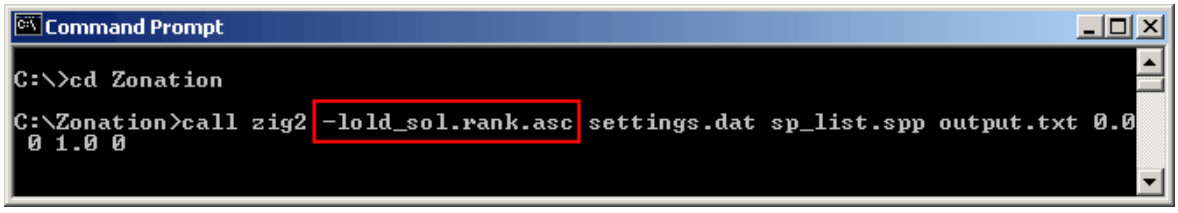
Using nested batch files is extremely useful when running many solutions using combinations of settings. For example, if we would use only one batch file to run the solutions described above, we would need to write a separate call for each of the nine solutions, and with many calls it is relatively to introduce errors into some of them:


do_zig2.bat - Notepad
File Edit Format Help
call zig2 -r settings1.dat species1.spp outS1_sp1 0.0 0 1.0 1
call zig2 -r settings1.dat species2.spp outS1_sp2 0.0 0 1.0 1
call zig2 -r settings1.dat species3.spp outS1_sp3 0.0 0 1.0 1
call zig2 -r settings2.dat species1.spp outS2_sp1 0.0 0 1.0 1
call zig2 -r settings2.dat species2.spp outS2_sp2 0.0 0 1.0 1
call zig2 -r settings2.dat species3.spp outS2_sp3 0.0 0 1.0 1
call zig2 -r settings3.dat species1.spp outS3_sp1 0.0 0 1.0 1
call zig2 -r settings3.dat species2.spp outS3_sp2 0.0 0 1.0 1
call zig2 -r settings3.dat species3.spp outS3_sp3 0.0 0 1.0 1

3.2.4 Loading previously calculated Zonation solutions

It is also possible to load previously calculated Zonation solutions. This is a useful utility, if you want to make some further analysis with your old solution, but also if you need to test the performance of your old solution in different circumstances (see section 3.6.6, solution cross-comparison using solution loading).

You can load solutions either from the command prompt or the windows interface. When operating the program from the **command prompt** type "-lfilename" as the second parameter of your call. "-l" points out that an old solution is loaded. For file name enter the name of the ranking file from your old solution (**.rank.asc file**, one of the output files produced during each run). Thus, a typical call when loading an older solution would look like this:



Remember to give a new output name in the call, if you do not wish to overwrite your old solution. If you are using the **windows interface**, select the "Load old solution .rank file" -option from the **Run settings -window** and type the name of your rank file on the field below. Give the name of your species list file and adjust the settings if needed.

3.3 Input files & settings

3.3.1 Introduction

To use the Zonation software, you need a set of input files, some of which are compulsory, some optional. You can use some of the tutorial files as templates when creating your own input files. All of these are text files (technically ASCII files), but to separate different types of files from each other, it is useful to give an additional suffix to your input files.

© 2004-2006 Atte Moilanen

.asc files This is the suffix for all basic GIS raster files such as species distribution layers, cost layers, mask file or uncertainty map layer. All these files need to be exported from a GIS software (e.g. from ArcView) or produced with some other appropriate software. When exporting, remember to select ASCII as the file format. During the export, the suffix will be automatically added after the file name.

.spp files A suffix for species list files such as species list file or uncertainty analysis weights file. In Zonation, these files would contain a list of .asc files with possible parameters. You need to create all .spp files yourself, for example, with Notepad. You can use the tutorial files as templates. When saving a .spp file, remember to add the suffix (.spp) after the file name.

.dat files This is the suffix used in the tutorial and examples for the run settings file. Also this file needs to be created by yourself. You can use the tutorial files as templates. When saving the file, remember to add the suffix (.dat) after the file name.

Note that you could call .spp and .dat files anything, e.g. myspecies.spp or myspecies.txt, but using consistently a unique extension helps you in organising and finding files of the required type.

3.3.2 Compulsory files

All these files are needed every time you run Zonation.

3.3.2.1 Species distribution map files

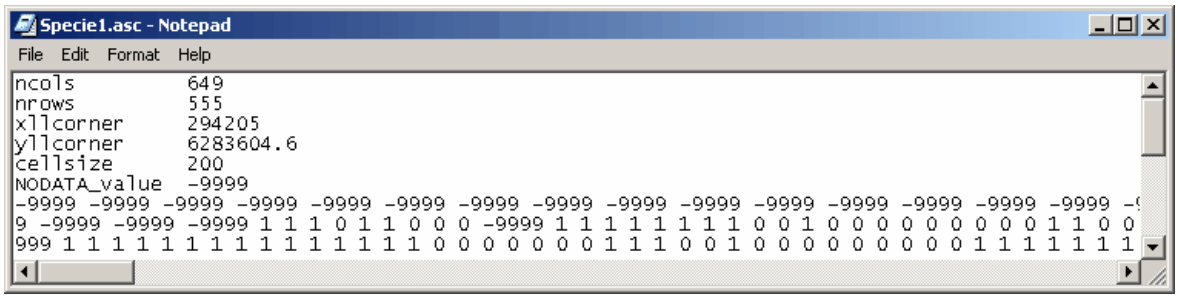
A standard GIS raster file (.asc -file) of species distribution, one file per each species. These files need to include the standard GIS raster fill header:

`ncols`	Number of columns
`nrows`	Number of rows
`xllcorner`	X-coordinates of the low-left corner
`yllcorner`	Y-coordinates of the low-left corner
`cellsize`	Cell size used in the raster file
`NODATA_value`	Definition of "no data" values. In example files "no data" has either value -1 or -9999.

After these rows comes the species distribution matrix. Each value in the matrix describes species occurrence in a specific cell. Values can be of any form of data, e.g. probability of occurrence, presence/absence -data, number of population etc. as long as the data is in same format across all species distribution files. Note that value 0 in the matrix indicates that the species does not occur in the cell with certainty, whereas lack of data must be marked as -9999 or with a similar value indicating "no data".

It is important that all species distribution rasters have the same grid size! **This means that in all files the number of columns and rows as well as the size of cells should be equal**. It is equally important to have **at least one row of no data on each edge of the raster matrix**. This is due to computational reasons and the lack these no data -rows leads to a situation where the program automatically transforms the values on edge rows to missing data. This inturn alters the species distribution information. Missing data in the species distribution rasters do not necessarily need to be congruent between all species, the program will run if cells marked as "no data" for one species has values for other species. However, if missing data is not aligned, there are implications for the use of the BQP. Remember also to use **decimal points, not commas**, in all the input files.

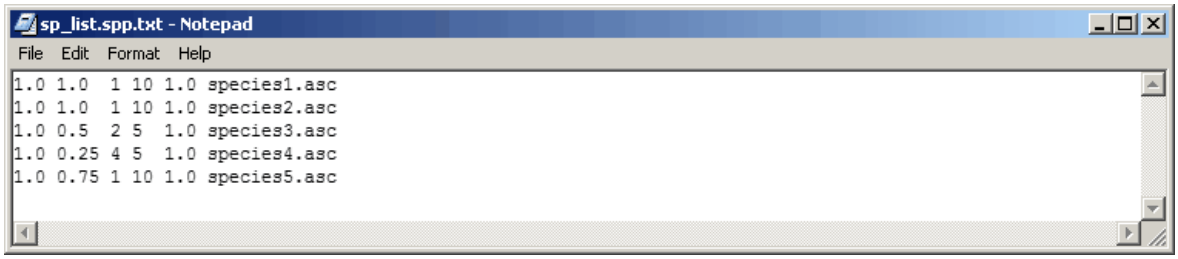
© 2004-2006 Atte Moilanen



Picture of species distribution map file.

3.3.2.2 Species list file

A .spp file containing a list of all species distribution map files (.asc -raster files), which will be used in your analysis. Each species file is on a separate row. This file always contains six columns:


sp_list.spp.txt - Notepad
File Edit Format Help
1.0 1.0 1 10 1.0 species1.asc
1.0 1.0 1 10 1.0 species2.asc
1.0 0.5 2 5 1.0 species3.asc
1.0 0.25 4 5 1.0 species4.asc
1.0 0.75 1 10 1.0 species5.asc

Picture of species list file.

1. Species weight ($\mathbf{w_i}$) in the Zonation algorithm. If no weights are used, this should be set to 1.0. In the example above all species have equal weights (1.0), but weights could go from zero to any positive value. No negative value can be used as species weight. Using 0 as a weight means, that the program calculates the performance of the species during cell removal, but that the species does not in any way influence the cell removal order. Thus, other species are acting as surrogates for weight-zero species. Note that species-specific weights have no influence on the analysis if you have chosen the target-based benefit function as your cell removal rule. This is because all species have given targets when using this cell removal rule - thus weights have no influence on the outcome.

2. The α -value of species-specific scale of landscape use (parameter of negative exponential, α_i). **This parameter is only needed when you are using distribution smoothing as a part of your analyses**. The value indicates how species use the surrounding landscape and can be calculated based on, for example, the dispersal capability or the home range sizes of the species. The α –value can be calculated as

$$\alpha = \frac{2 * [\text{Cell size in km}]}{[\text{Use of landscape (km)}] * [\text{Input cell size}]}$$

E.g. if the known/guesstimated mean dispersal capability of a species A is 3 km and the cell size in species distribution files is 1.0 km, then the value of α for species A is ~0.67.

$$\alpha = \frac{2*1}{3*1} \approx 0.667$$

The last part of the equation ([Cell size in km]/[Input cell size]) is needed to keep the α – **value in same unit of length as the cell size** given in the species distribution map file. E.g. if the cell size of previous example would be given in meters instead of kilometers (thus the cell size would be 1 000 m in the .asc files instead of 1 km), the α -value would be as follows:

© 2004-2006 Atte Moilanen

$$\alpha = \frac{2*1}{3*1000} \approx 0.00067$$

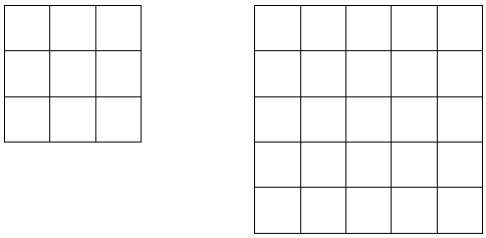
Another common unit used in raster files is degrees. Also these need to be converted to get the correct α -value. Let us assume that the cell size in our example was 0.0083 degree, equaling approximately 0.860 kilometers. Thus the α -value in this case is

$$\alpha = \frac{2*0.860}{3*0.0083} \approx 67.1$$

It is important to understand, that this parameter is NOT the same α -value as is used in uncertainty analysis! The two parameters only happened to be denoted with the same symbol in literature. Note also, that if distribution smoothing is not used, you should nevertheless enter a value in this column. This can be any positive number, e.g. a dummy value of 1. **Do not leave the column empty!**

Columns 3 and 4 together define the BQP (Boundary Quality Penalty) settings for the species. This info is only used if BQP is included in to the analysis. Note, that even if BQP is not used, you should nevertheless enter a value into these columns. They can be any positive numbers, e.g. a dummy values of 1. **Do not leave the columns empty!**

3. Row number in BQP definitions file linking the species to a correct penalty curve. This information is used only if you are using BQP as a part of your analysis.
4. Species-specific buffer size (number of cells). This is used only if you are using BQP as a part of your analysis. Buffer size indicates the area around the focal cell in which any fragmentation (removal of cells) influences the quality of the focal cell. For species with large home ranges the buffer size should be larger and for species with small home ranges a smaller buffer size is adequate.

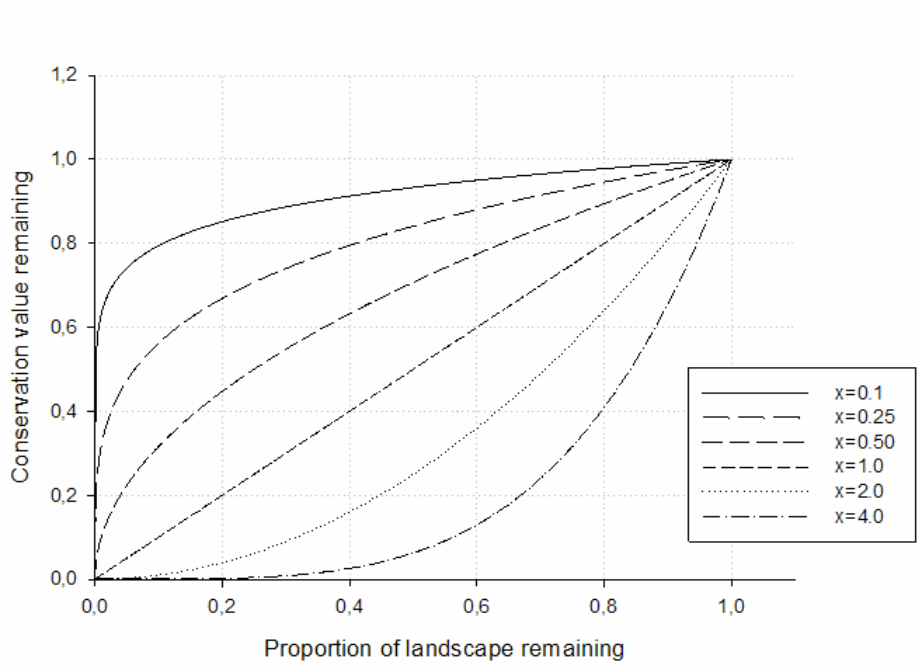


buffer size = 3 buffer size = 5

Column 5 is needed when using additive benefit function or target-based planning as your cell removal rule.

5. This column has two functions depending on which cell removal rule is used.
   - If you are using **additive benefit function** as your cell removal rule, this parameter is the exponent (**x**) of the species-specific power function ($\mathbf{r_i^x}$) that translates representation to value. The power function determines the rate of loss of conservation value from the remaining landscape as cells are removed. The exponent can be any positive number, but zero is not a valid value.

© 2004-2006 Atte Moilanen



Picture of power functions with differing x -values.

- If you are using **target-based planning** as your cell removal rule, this parameter determines the target proportion (from 0.0 to 1.0) of the species distribution, which you require in the final solution.

Note that even though benefit function or target-based planning is not used, you should nevertheless enter a value into this column. This can be any positive number, e.g. a dummy value of 1. **Do not leave the column empty!**

6. Name of the species distribution map file (.asc -raster file). If your species distribution maps are in a different directory than your species list file, remember also to type the correct path in front of the names.

When using the windows version, type the correct path of your species list file on the "Species file list in file" -box in "Run settings" -window (if all the files are in the same directory with Zonation program, only the name of the file is requiered).
If you are running the program from command prompt, type the name of your species list file as the third parameter on the command row.

Note that the `FOR`-command can be used in creative ways to automatically create species list files. For example, the following single command row, typed and run from the command prompt,

```
FOR /L %i IN (1,1,900) DO @ECHO 1.0  1  1  1  0.25  p%i.asc >> my_spp_list.spp
```

generates a file my_spp_list.spp, which has rows and relevant parameters for files p1.asc, p2.asc, ..., p900.asc. The ">>" at the end of the command indicates redirection of output into the following file. Without the ">> my_spp_list.spp", output is shown on the screen (command prompt).

Another variant of the for command allows one to loop through a set of files using the normal wildcard file name specification:

```
FOR %i IN (species_*.asc) DO @ECHO 1.0  1  1  1  0.5  %i
```

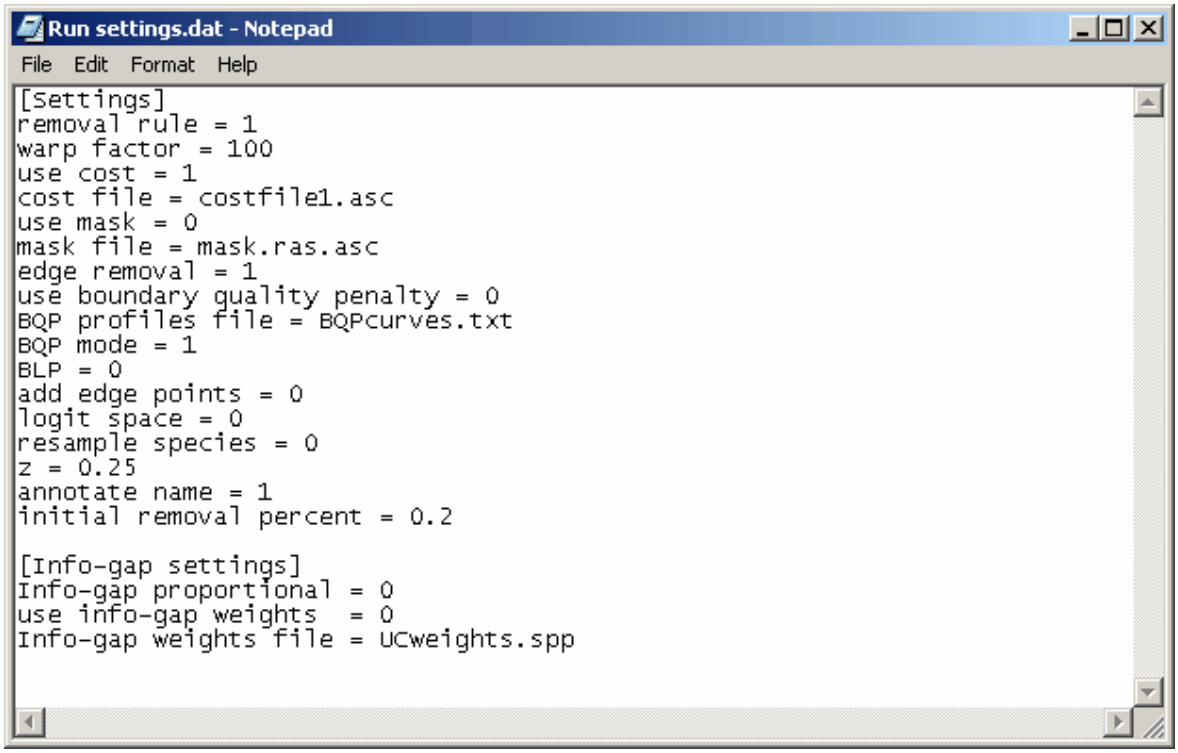
See the help for the `FOR`-command for further information.

There should not be any empty rows at the end of the species list file. If necessary, you can enter comments in your species list file on separate rows starting with the symbol #. Remember also to use **decimal points, not commas**, in all the input files.

© 2004-2006 Atte Moilanen

3.3.2.3 Run settings file

A .dat file containing all basic Zonation and info-gap uncertainty analysis settings. **This input file is needed only when running the program from the command prompt**. When running from the windows interface these same settings can be found on the "Run settings" -window. In the run settings file the following parameters need to be written on separate rows:


Run settings.dat - Notepad
File Edit Format Help
[Settings]
removal rule = 1
warp factor = 100
use cost = 1
cost file = costfile1.asc
use mask = 0
mask file = mask.ras.asc
edge removal = 1
use boundary quality penalty = 0
BQP profiles file = BQPcurves.txt
BQP mode = 1
BLP = 0
add edge points = 0
logit space = 0
resample species = 0
z = 0.25
annotate name = 1
initial removal percent = 0.2
[Info-gap settings]
Info-gap proportional = 0
use info-gap weights = 0
Info-gap weights file = UCweights.spp

Picture of settings file.

[Settings]

cell removal rule — Determines which cell removal rule will be used. 1 = Basic core-area Zonation, 2 = Additive benefit function, 3 = Target-based planning.

warp factor — Defines how many cells are removed at a time. If warp factor is 100, it means that 100 cells are removed at each iteration. Thus a lower warp factor leads to a finer solution, but also to an elongated running time, whereas a high warp factor keeps the running time short, but might result in a more coarse solution. If the warp factor is more than 1% of the remaining cells, then only 1% is removed. For example, if there are only 100 cells remaining in the landscape, then only one cell can be removed regardless of what the warp factor is. [In our tests having a warp factor of 100 has had little influence on the solution compared to lower warp factor values, but the run times have been considerably shorter. We recommend to use a warp factor of 1 mainly for the final runs, if run times allow it. You can compare the effects of different warp factors with Landscape comparison.]

use cost — Determines whether land costs are included in the analysis (value = 1). If no land costs are used, this parameter should be set to 0.

cost file — Indicates which land cost file will be used.

use mask — Determines whether a removal mask layer is used (value = 1) or not (value = 0).

© 2004-2006 Atte Moilanen

mask file Indicates which mask layer file will be used.

edge removal Determines whether the program removes cells from the edges of areas (value = 1) or anywhere from the areas (value = 0). Note that setting this parameter to 0 might increase the running time substantially with large landscapes.

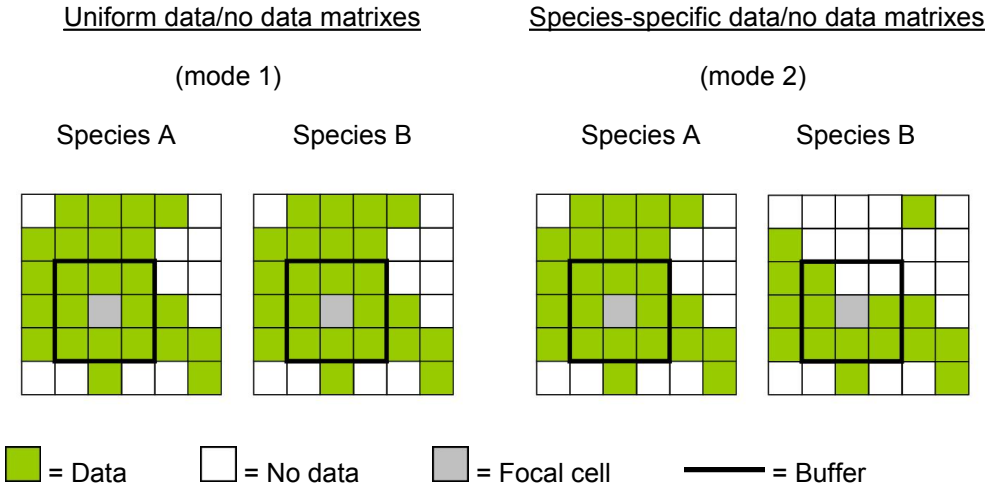
use boundary quality penalty Determines whether BQP is used (value = 1) or not (value = 0). Use of BQP leads to more aggregated solution. BLP, BQP and distribution smoothing probably should not be used at the same time due to difficulties in interpreting results.

BQP profiles file Indicates which BQP profiles file will be used.

BQP mode Determines how the program will calculate the effects of fragmentation from species distribution data. Essentially, this parameter tells the program what type of species distribution layers you are using.

Mode 1 indicates that the data/no data matrix in all species distribution map files should be uniform and aligned, and that there are no differences between species in terms of which cells are considered potential habitat, and which are then used in BQP buffer calculations. In other words, all species would be dependent on the same general habitat type, such as forest. With mode 1, Zonation automatically aligns missing data if different species layers happen to have missing data at different locations. When aligning data, if species A has missing data at location (x,y) where any species B has a positive occurrence, then the missing value for species A is replaced by a zero.

Mode 2 indicates that the data/no data matrixes are not uniform and aligned, and that the program needs to calculate species-specific buffers for each species/cell separately. Mode 2 is more realistic in the sense that fragmentation/loss in habitats that are not suitable for the species will not influence the value of the focal cell. But, mode 2 also requires longer computation times due to more complicated species-specific calculations. Also, use of mode 2 at least doubles the memory usage of Zonation, thus decreasing the number of species that can be run in one analysis. Thus, mode 1 is a preferable when all species use approximately the same habitat type.



© 2004-2006 Atte Moilanen

BLP

Defines a penalty given for the boundary length of the reserve. Use of BLP leads to more aggregated solution. Try first a small value, e.g. 0.01, to perceive the effect of BLP to the solution. **When including BLP in the analysis, always use a warp factor of 1**. If BLP is not used, this parameter should be set as 0. BLP, BQP and distribution smoothing should not be used at the same time due to difficulties in interpreting results.

add edge points

Randomly selects additional cells inside the landscape that will be initially classified as edge-cells, from which removal can proceed. The value of this parameter determines the number of cells that are selected.

logit space

Determines whether the biological values of cells will be transformed from logit space (value = 1) for processing. In this case the raster files (.asc files) should contain the values of the linear predictor part of a logistic regression. If data is not to be transformed from logit space, this parameter should be set as 0.

resample species

This option allows you to, for example, test analyses using only a subset of species. The program selects an random set of species from your species list file and uses them to run the analysis. Thus you can run several analyses and check how the selection of species influences the outcome. Note that the random sets do not include multiple selections of one species, all species in the set are different ones. To use this option enter the number species you wish to include in the set. If this value is zero, any negative value or equal to the total number of species, no sampling is done.

z

This value is used to calculate the extinction risks of species as their distribution sizes are decreasing. z is the exponent of the species-area curve ($S = cA^z$), which has been widely used in ecological studies. In theory, you can give z any positive value, but as a default it has been set to a commonly found empirical value $z = 0.25$.

annotate name

With this option you can mark your output file names to show which analyses have been used to produce them (value = 1). The program will add letters and numbers in the middle of your output file name depending on the used analyses:

CAZ_/ABF_/TBF_ = shows, whether you have used the basic core-area Zonation (CAZ), the additive benefit function (ABF) or the target-based function (TBF) as your cell removal rule.
M = mask used.
C = costs used.
E = edge removal used.
A = edge points added.
Sxxx = distribution smoothing used. The following numbers show the factor that has been used to multiply the species-specific α –values. Note that for output the factor has been multiplied by 100. Thus using factor = 1.0 would result a suffix of S100, factor = 0.1 results a suffix of S10 etc.
IGxxx = uncertainty analysis included. Again the following numbers show the info-gap α –value multiplied by 100.
BQP = BQP included.
BLPxxxx = BLP included. Again the following numbers show the penalty given for the boundary length multiplied by 1 000. I.e. using BLP = 0.5 results a suffix of BLP500, BLP = 0.05 results a suffix of BLP50 etc.

© 2004-2006 Atte Moilanen

If you do not wish to use this option, the parameter should be set as 0.

`initial removal percent` Defines the worst proportion (from 0 to 1) of the landscape that is removed in the beginning of the procedure to create more edges in the landscape. Obsolete, preferably use "add edge points" above.

`[Info-gap settings]`

These settings are required, if you are including uncertainty in species distributions into your analysis.

`Info-gap proportional` Determines whether the errors in species occurrences are uniform errors (value = 0) or proportional errors (value = 1). Uniform error is the default setting and works for most of the data sets, but in some cases it is more appropriate to use proportional errors (see e.g. Ben-Haim 2001).

`use info-gap weights` Determines whether species-specific distribution uncertainty map layers are used in the info-gap analysis (value = 1) or not (value = 0).

`Info-gap weights file` Indicates which uncertainty analysis weights file will be used.

It is very important that all the parameters in your run settings file are written **exactly** like presented here. If there are errors in the spelling of parameters, the program can not find them and will use default settings instead. The order of parameters on the other hand is not obligatory. If necessary, you can enter comments in your species list file on separate rows starting with the symbol #. Remember also to use **decimal points, not commas,** in all the input files.

When adjusting the settings, it is good to understand the differences between **Initial removal**, **Edge removal** and **Add edge points** options. Initial removal was originally developed to remove areas that were known to be poor in biological value (e.g. towns, roads etc.) and to increase the number of edge cells. Hypothetically, this option could have been useful in cases where a large area of "poor" habitat is completely surrounded by "good" habitats, and the Zonation program should first remove all the good habitats from the edge to reach the poor area. Naturally, by not selecting the edge removal option the program would easily find all poor habitats deep inside the landscape, but when working with large datasets (which often is the case) edge removal is needed to keep the computation times realistic. However, using initial removal has it downside. If the amount of landscape which is initially removed is not carefully defined, this might result in loss of biologically valuable areas (not necessarily the most valuable areas, but areas that might have a high value for the structure of reserve network or for the protection of certain species). Thus the program would not be able to calculate the most optimal solution for the respective landscape.

To prevent any valuable areas to be lost and to keep the computation times short, it is recommended that one should use the add edge points option together with edge removal. By adding edge -like cells into the landscape the program can spot any poor areas surrounded by good habitats without the risk of removing valuable cells.

3.3.3 Optional files

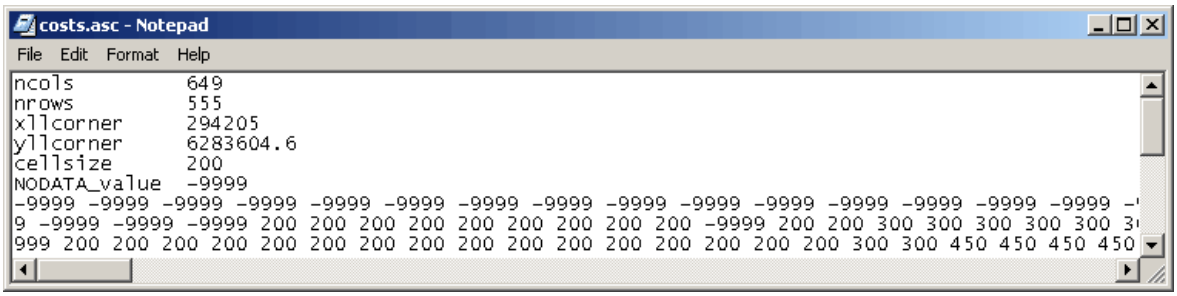
These files are needed only when certain options are used.

3.3.3.1 Cost layer

A standard GIS raster file (.asc -file) on land cost information**.** This file includes all basic raster information as explained in species distribution map files and a matrix of land costs in each cell.

© 2004-2006 Atte Moilanen

The land cost value in the matrix can be any positive number larger than 0. Thus, zero nor any negative value can not be used as land cost! If areas with no land costs need to be included in the analyses, the land cost value for these cells can be set very low, e.g. 0.00001. Note that here the costs do not need to be measured in terms of money, you can use other measures of economical loss as well. For example in economical fisheries the fishing intensity of a landscape can be used as a cost layer - the higher the fishing intensity, the higher is the cost of protecting the particular site. The cost layer is an optional file, the program can be run without cost data as well. If land costs are not included in the analysis, all cells implicitly have an equal cost value of 1.



Picture of cost layer file.

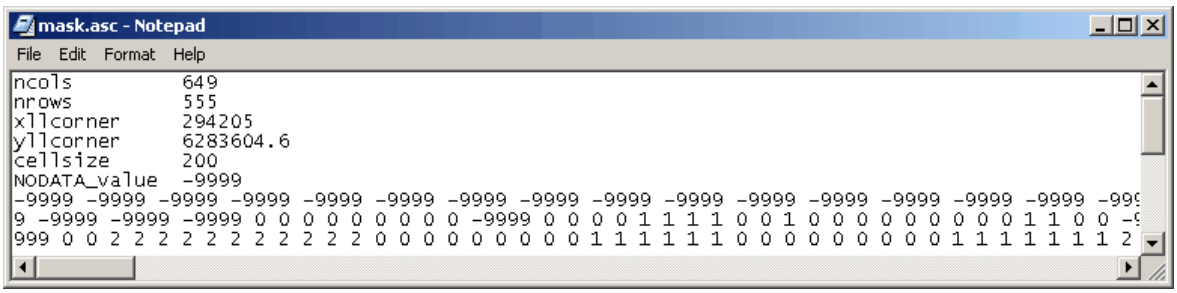
It is important that the cost layer raster has the same grid size as the species distribution map rasters! **This means that in all files the number of columns and rows as well as the size of cells should be equal**. It is equally important that all those cells which have data of any of the species used in the analysis (that is to say, the cells that are NOT marked as "no data" in species distribution files), also have to have a cost value. Otherwise undefined program behaviour may occur. Remember also to use **decimal points, not commas**, in all the input files.

When using the cost layer, remember to type in to your Run settings -file "`use cost = 1`" (cost option selected) and "`cost file = yourcostfile.asc`" (name of your cost layer file). If you are running the program from windows version, go to "Run settings" -window, select the "Use cost information" -option and type the correct path to your cost layer file (if the file is in the same directory with Zonation program, only the name of the file is required).

3.3.3.2 Removal mask layer

A standard GIS raster file (.asc -file) which determines the removal hierarchy of the edge cells. The main use of the mask layer is **replacement cost analysis** (see section 3.5.5). This file includes all basic raster information as explained in species distribution map files, followed by a matrix, where cells are categorized as follows:

0. Cells with a value of 0 are considered as "normal" cells with no preference to removal hierarchy. These cells will be removed from the edges after there are no more cells with a value of 2 left.
1. Cells with a value of 1 are removed last from the edges. These cells may, for example, have a special conservation value or they may already be ear-marked for conservation. These cells will be removed only after there are no more cells with values of 0 or 2 left on the edges and are therefore most likely included in the final solution.
2. Cells with a value of 2 are removed first from the edges. These cells may be, for example, undesirable for conservation (e.g. built-up areas, private areas, areas ear-marked for residential building or commercial fishing etc.) or they may have any other reason to be primarily excluded from the final solution.



© 2004-2006 Atte Moilanen

Picture of removal mask layer file.

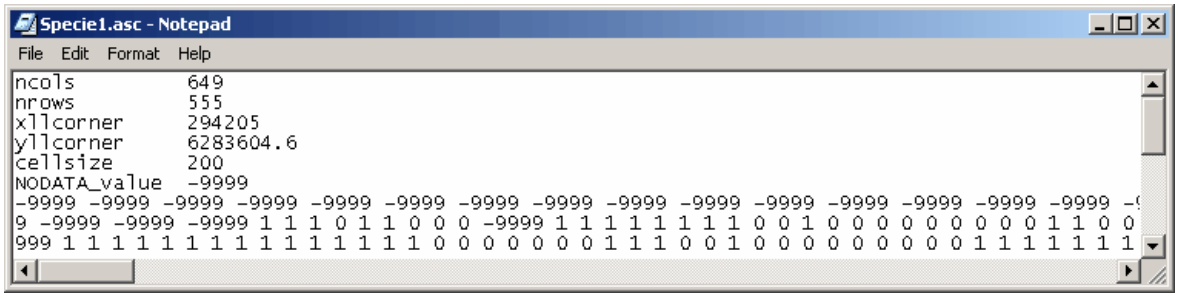
It is important that the mask layer raster has the same grid size as the species distribution map rasters! This means that in all files the number of columns and rows as well as the size of cells should be equal. It is equally important that all those cells which have data of any of the species used in the analysis (that is to say, the cells that are NOT marked as "no data" in species distribution files), also have a mask value. Otherwise undefined program behaviour may occur. Remember also to use **decimal points, not commas**, in all the input files.

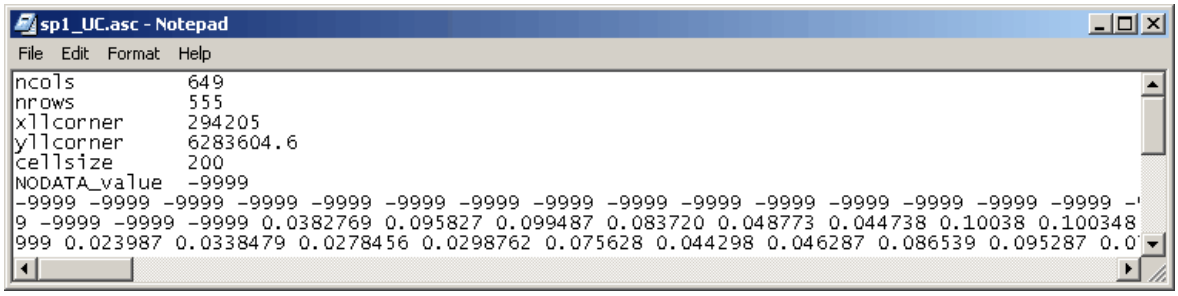
When using the removal mask layer, remember to type in to your Run settings -file "`run mask = 1`" (mask option selected) and "`mask file = yourmaskfile.asc`" (name of your removal mask layer file). If you are running the program from windows version, go to "Run settings" -window, select the "Use incl./excl. mask" -option and type the correct path to your removal mask layer file (if the file is in the same directory with Zonation program, only the name of the file is required). Note that use of removal mask layer is likely to result a biologically non-optimal solution as the program is not allowed to remove cells only based on their conservation value. See **Replacement cost analysis** (section 3.5.5) for the analysis of the suboptimality of masked solutions.

3.3.3.3 Distributional uncertainty map layer

A standard GIS raster file (.asc -file) of uncertainties in species occurrence. **These files are needed if you are including the uncertainty in species distributions in to your analysis,** where you need one uncertainty map layer for each species used in the analysis. The file includes all basic raster information as explained in species distribution map files and a matrix of species occurrence uncertainties in each cell (parameter $\mathbf{w_{sc}}$ in the info-gap uncertainty model). The species-cell-specific uncertainty value w_{sc} can be any measure of error in prediction, or any uncertainty about whether the species will persist there, or a combination of those, as long as the data of all species is in same format.

For example, if confidence intervals are available for the probabilities of occurrence of species A in a given cell, the uncertainty value for species A in that same cell can be the size of the (lower half of the) respective confidence interval. Or the probabilities of anthropogenic threat, e.g the uncertainty of occurrence of species in a given cell due to human activities in the near by future, can be used as uncertainty value. Or both. The higher the uncertainty value, the greater the risk that the species does not actually occur there (although the species distribution data might suggest so). Thus, an uncertainty value of 0 indicates that the observed occurrence of a species A in a given cell is trusted to be completely accurate. Note that the uncertainty values should not be negative values.





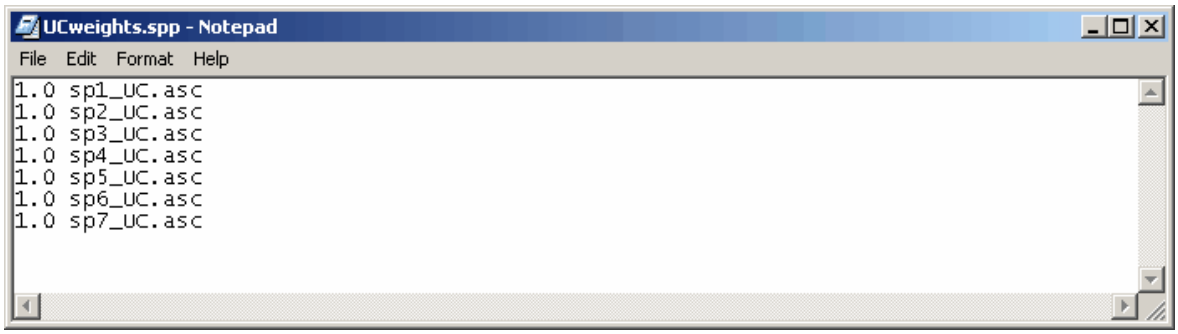
Picture showing both the species distribution layer (species1.asc) and the uncertainty layer (sp1_UC.asc) for species 1. During the distribution discounting process the value in each cell of the distribution layer will be discounted by a multiple of the corresponding value in the uncertainty layer.

© 2004-2006 Atte Moilanen

It is important that the uncertainty layer raster has the same grid size as the species distribution map rasters! **This means that in all files the number of columns and rows as well as the size of cells should be equal**. It is equally important that all those cells which have data of the species occurrence (that is to say, the cells that are NOT marked as "no data" in the respective species distribution file), also have to have an uncertainty value. Otherwise undefined program behaviour may occur. Remember also to use **decimal points, not commas**, in all the input files.

3.3.3.4 Uncertainty analysis weights file

A file containing a list of all distributional uncertainty map layers (.asc -raster files) with each species file on their own row. **This file is needed if you are including the uncertainty in species distributions into your analysis.** This file always contains two columns:



Picture of uncertainty analysis weights file.

1. **Species-specific weights in the uncertainty analysis**. With these you can stress the accuracy of occurrence of a certain species (e.g. very rare species). The higher the weight, the more strongly the program prefers cells with low uncertainty. Species-specific weights can have any positive value larger than 0. Thus, zero or negative values cannot be used as weights. If no species-specific weighting of uncertainty is used (as is most commonly the case), this should be set as 1.0

2. Name of the **species distributional uncertainty map layer**. If your uncertainty maps are in different directory than your weights file, remember also to type the correct path in front of the names. **Note that the uncertainty layers for species have to be in the same order as the species distribution maps in the species list file!**

When using the windows version, select the "Use info-gap distribution discounting" -option in "Run settings" -window (under Info-gap settings) and type the correct path of your uncertainty analysis weights file on the field.
If you are running the program from command prompt, remember to type the name of your uncertainty analysis weights file to your Run settings -input file ("`Info-gap weights file = yourweightsfile.spp`") under the Info-gap settings.

Note that there shouldn't be any empty rows at the end of the uncertainty analysis weights file. This is because the program might interpret these as empty values or files that just don't have any names. Remember also to use **decimal points, not commas**, in all input files.

3.3.3.5 Boundary quality penalty definitions file

A text file where different species responses to neighbourhood habitat loss are displayed as points of penalty curves, each curve on their own row.

© 2004-2006 Atte Moilanen

BQPcurves.txt - Notepad

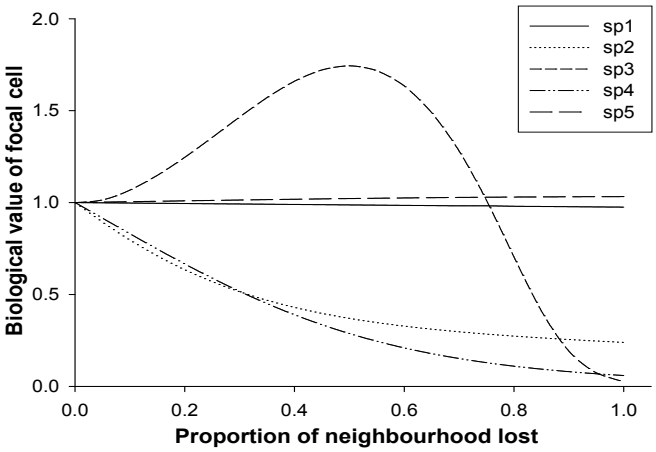
File Edit Format Help

1	1.0000	1.0000	0.9500	0.9987	0.9000	0.9975	0.8500	0.9962	0.8000	0.9949	0.7
2	1.0000	1.0000	0.9500	0.8926	0.9000	0.7953	0.8500	0.7089	0.8000	0.6336	0.7
3	1.0000	1.0000	0.9500	1.0142	0.9000	1.0676	0.8500	1.1480	0.8000	1.2460	0.7
4	1.0000	1.0000	0.9500	0.9147	0.9000	0.8298	0.8500	0.7464	0.8000	0.6656	0.7
5	1.0000	1.0000	0.9500	1.0024	0.9000	1.0048	0.8500	1.0071	0.8000	1.0095	0.7
6	1.0000	1.0000	0.9500	1.0021	0.9000	1.0043	0.8500	1.0064	0.8000	1.0086	0.7
7	1.0000	1.0000	0.9500	1.0154	0.9000	1.0291	0.8500	1.0406	0.8000	1.0494	0.7

Picture of BQP definition file.

Here, the first column indicates the number of row. After row numbers comes the first column pair, in which the initial state (when no neighbourhood habitat has been lost) is represented. Here, the first number of the pair indicates the proportion of neighbourhood habitat left and the second column indicates the status of biological value in the focal cell. Hence, in the initial state, when no habitat has yet been lost and therefore the biological value of the focal cell has not yet changed, the two parameters always have a value of 1.000, respectively. The following column pairs describe the loss of neighbourhood habitats and effects that this has on the biological value in the focal cell. Note that the change in biological value can be either negative (< 1) or positive (> 1) depending on species preference to fragmented habitats.

As mentioned earlier, the column pairs should be considered as x,y -coordinates on a penalty curve. To draw a penalty curve, or any curve at all, you need to have at least two points. Thus, in the BQP definition file at least two column pairs are needed. The two points could for example be the initial point, when no habitat has been lost and the final point, when all the habitat has been lost. E.g. for species A the two points could be (1.000 1.000) and (0.000 0.500), meaning that when all the neighbourhood habitat has been lost, the biological value of the focal cell for the species has decreased by half. Presently, each of the penalty curve rows can contain a maximum of 20 points!



The figure above represents an example of different species-specific penalty curves (from Moilanen & Wintle 2006). Note that the curve increasing over value 1 indicates a species that prefers semi-fragmented habitats.

© 2004-2006 Atte Moilanen

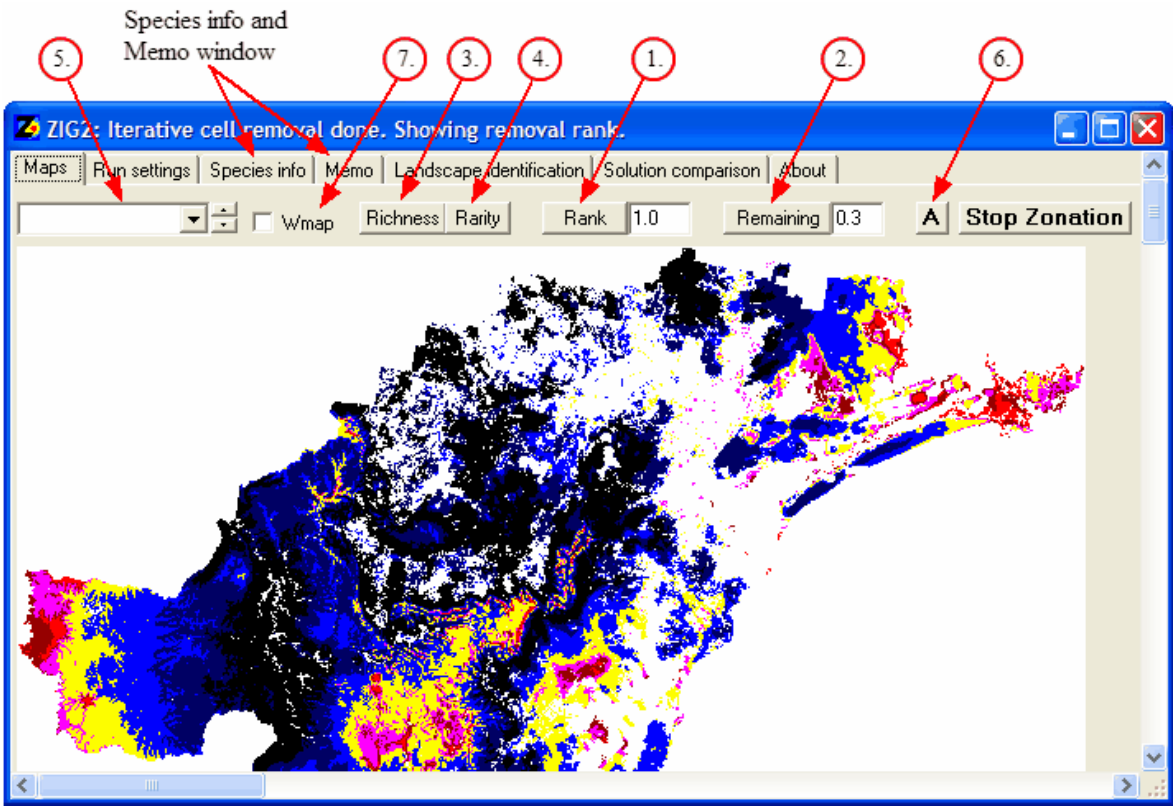
3.4 Standard Zonation output

Next we will describe the basic output produced by the program. Running Zonation automatically produces two sets of outputs:

1. **Visual output** in the windows interface.
2. **File output**. These files will be saved in the same directory as the program unless you have specified another path for your output.

3.4.1 Visual output

Maps -window

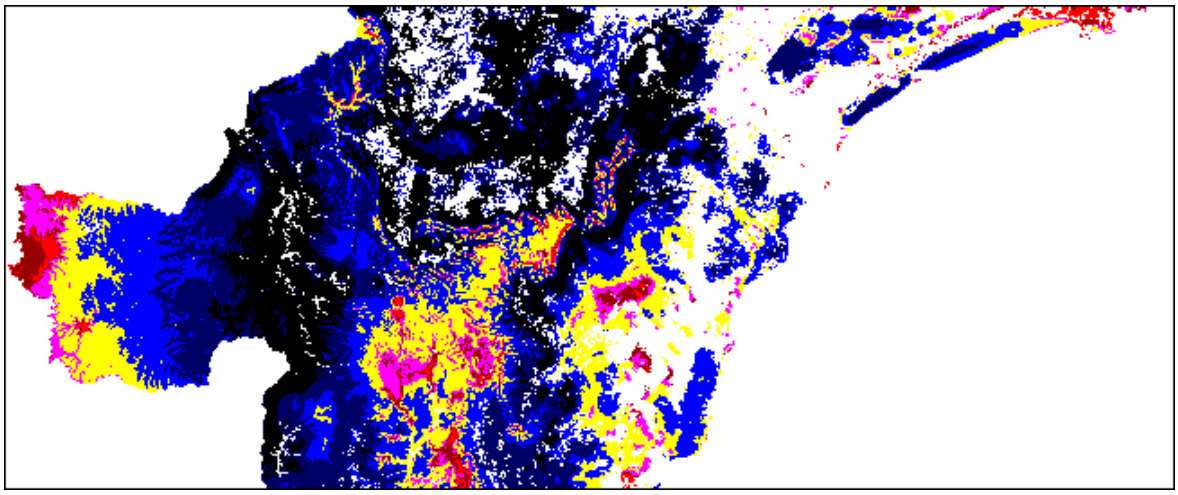


Picture of the "Maps" -window after the program has finished running.

1. **Rank.** In the "Maps" -window the first map that appears (and the creation of which you can follow on screen during the iterative cell removal) is the ranking of the landscape. In the picture sites are ranked by using different colours to indicate the biological value of the site:
   - red = the best 2 % of the landscape
   - dark red = the best 2-5%
   - magenta = the best 5-10%
   - yellow = the best 10-25%
   - light blue = the best 25-50%
   - dark blue = the best 50-80%
   - black = the best 80-100% (or least valuable 20%)

   The information of this map is equal to the .rank.asc file that the program produces as part of file output. This map will also automatically be saved as a picture (output.jpg and output.emf files), but you can save it again (e.g. with a different name or to a different directory) by double clicking the picture. If a certain proportion of the landscape has been removed initially (see section 3.3.2.3 for "Initial removal"), that area is shown in black and is combained to the worst 20% of the landscape (see above, best 80-100% of the landscape). The background, i.e. the cells for which no data exists, are shown in white.

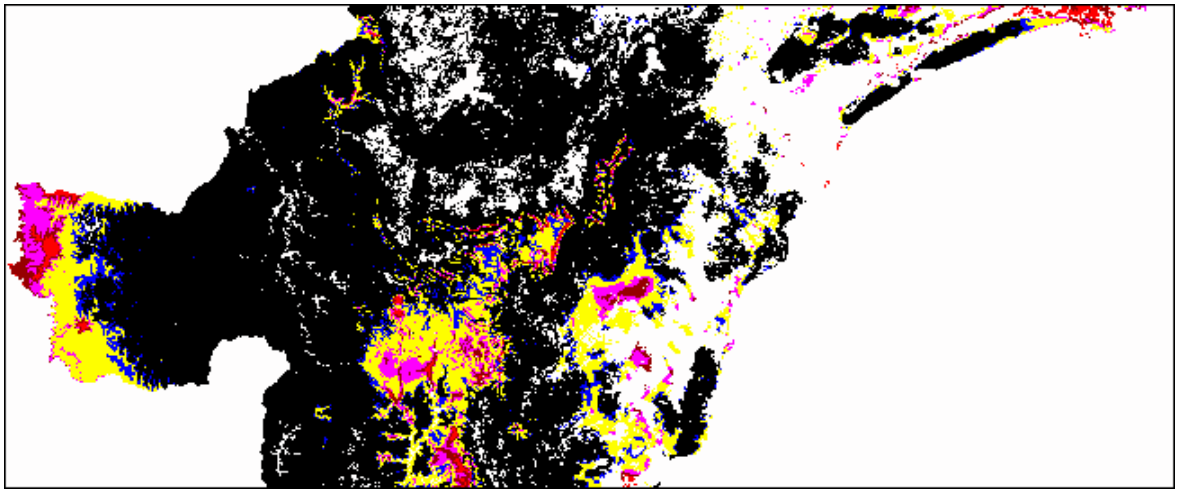
© 2004-2006 Atte Moilanen



A picture of the landscape ranking map.

In the options it is also possible to select a certain proportion of the best landscape based on the ranking, e.g. the best 10%. Type the wanted proportion (from 0 to 1) into the "Rank"-field and press the "Rank" button. The area removed after this procedure is shown in black and the best remaining area is shown in gradual colours. Note that you can also use this option to show you the worst proportion of the landscape. For example, if you select the best 90% (0.9) of the landscape, the area shown in black equals to the worst 10% etc.

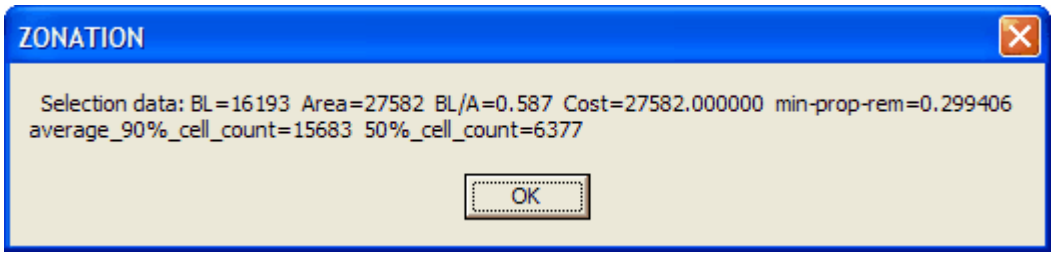
2. **Remaining.** In some cases it can be useful to find out those areas that are required for representing a certain proportion of species distributions. For example if you have a conservation target of protecting 10% of all species distributions, this can be done by typing the target proportion (here 0.1) in to the "Remaining"-field and pressing the "Remaining" button. **Note that using this option changes the colouring of the map**: Here the red colour does not present the best 2% of the landscape, but those areas that are needed to protect at least 2% of all distributions, and so on. It is equally important to understand that in this procedure the program displays areas that achieve at least the given target for all species simultaneously. Thus, other species may have higher proportions of their distributions remaining in the solution.



Here in gradual colours is shown the area required for representing at least 30% of distributions of all species. In black are those areas which are not included in the solution.

When a certain proportion of the landscape is selected based on either "ranking" or "remaining", the program displays a small information window about the selected top fraction. This window includes the following information:

© 2004-2006 Atte Moilanen



BL = Boundary length of the selected area.
Area = Count of cells in selected area.
BL/A = (Boundary length)/Area -ratio.
Cost = This will tell you, how much the selected area costs if you are using a cost layer. If no cost layer is used, all cells are given a equal value of 1 (thus, this will show the number of cells required for the area).
min-prop-rem = The proportion of distribution remaining in the selected area for the worst-off species (note that other species may have larger proportions remaining).
average_90%_cell_count and **50%_cell_count** = These numbers will tell you how many cells are required to represent on average 90% (50%) of the species distributions that are located in the selected area. We illustrate the 90% (50%) cells statistic with the following example. Assume you select a Zonation solution top fraction that includes at least 30% for the distributions of all species (that is Remaining = 0.3). Although for species A the selected area covers 40% of its original distribution. Now the 90% cells statistic is asking for 90% of the 40% = 36% of original remaining. To get the number of cells, the occurrences of species A are first ranked into decreasing order of occurrence density in the selected area. Note that species A does not occur in all cells in the landscape. It follows that if species A is widespread, getting the 36% could require, for example, 10000 cells from the selected area, whereas if species A has a limited distribution, 36% could mean 2000 cells. Note that the 90% (50%) statistic reports **the averages** of these numbers across all species used in the analysis.

		.19	.17	.20	.18	.16			.08	.14	.21	.67	.90	.70	.66	.56
	.18	.20	.20	.20	.15					.12	.33	.42	.70	.67	.65	.37
	.29	.38	.35							.03	.08	.10	.37	.65	.57	.25
	.26	.48	.32						.15					.25		
		.26														

Figure illustrating the example. Species A original distribution is marked with green cells (values indicating the probability of occurrence in each cell). The red line outlines the area required to retain at least 30% of all species distributions, here including 40% of species A distribution. The yellow cells show the area of 90% cell count **for species A**, totaling the 36% of species A original distribution.

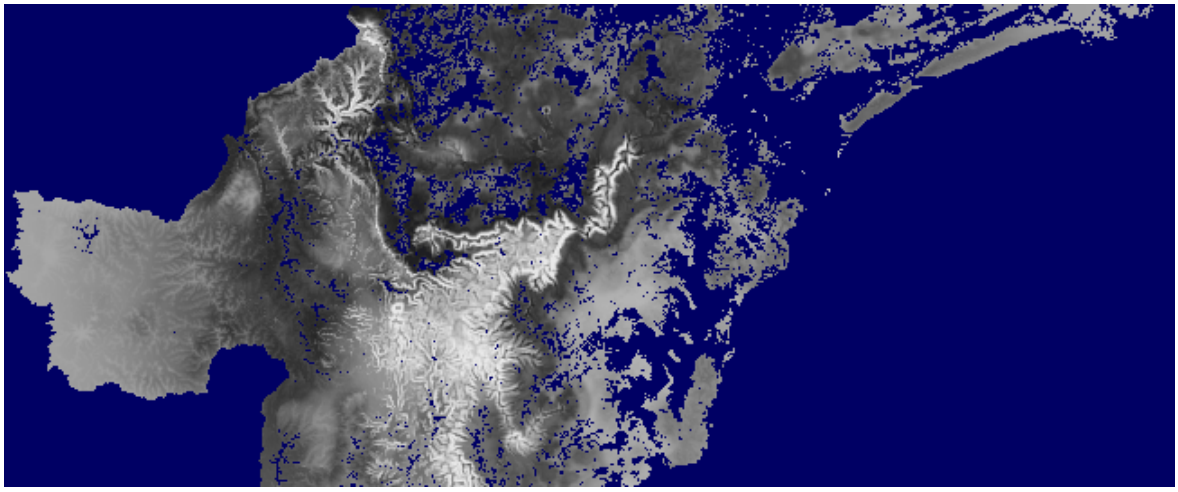
What is this statistic useful for then? It actually quantifies differences between cell removal rules. The trend is this: to get a given minimum fraction across species core-area Zonation requires more cells than the benefit function variants. This is because benefit function variants take occurrences as additive whereas core-area Zonation prefers the locations with very highest occurrence levels. However, if one investigates the number of cell needed to get the distribution for an individual species, then core-area Zonation may require fewer cells because it prefers the higher-quality (density) cells. Thus, benefit function variants generate landscapes with many species occurring simultaneously at potentially low occurrence levels and with high overlap between species. Core-area Zonation produces solutions with species occurring at higher densities, but with less overlap between species. Which kind of solution is preferable depends on the goals

© 2004-2006 Atte Moilanen

of planning, but it is important to realize that there may be significant differences between core-area Zonation and benefit function Zonation solutions.

3. **Richness.** By clicking on the "Richness" button you can highlight areas that have the highest occurrence values (in terms of fractions of distributions in the cell) across all species in your data. Here the colours indicate the sum of all normalized species distribution values in a given cell. In other words, the white areas represent those cells which have the highest proportional occurrence for the largest number of species.

4. **Rarity.** This option shows you the areas that are most important for any single species, in other words the core areas of a species distribution. These areas might have a low biodiversity (low number of species), but a very high occurrence of one species. Note the difference between rarity and richness maps: areas can have a high conservation value by containing cells that are either good for many species combined (richness) or the most important for a single species (rarity). Both species richness and rarity maps are in grey scale.



This is an example of a rarity map, where whiter areas show the core areas of species distributions. Areas with no data are shown in blue.

5. **Species-specific maps.** All maps explained above are summaries over all species. From the dialog box in top-left corner of the map window you can select species-specific maps showing the input distributions of species. To return to summary maps just click any of the map buttons (Rank, Remaining, Richness or Rarity).

6. **Annotations.** For printing your maps you can change the settings of the map layout in annotations by clicking the "A" button. You can adjust the colours of your maps, add scale line and panel ID, or just outline the landscape to distinguish it from the white background. After adjusting the layout settings, select again any of the map options (Specie-specific maps, Rank, Remaining, Richness or Rarity) and your new annotations will appear in the map window. To save any of the images just double click on the pictures and a saving window appears.

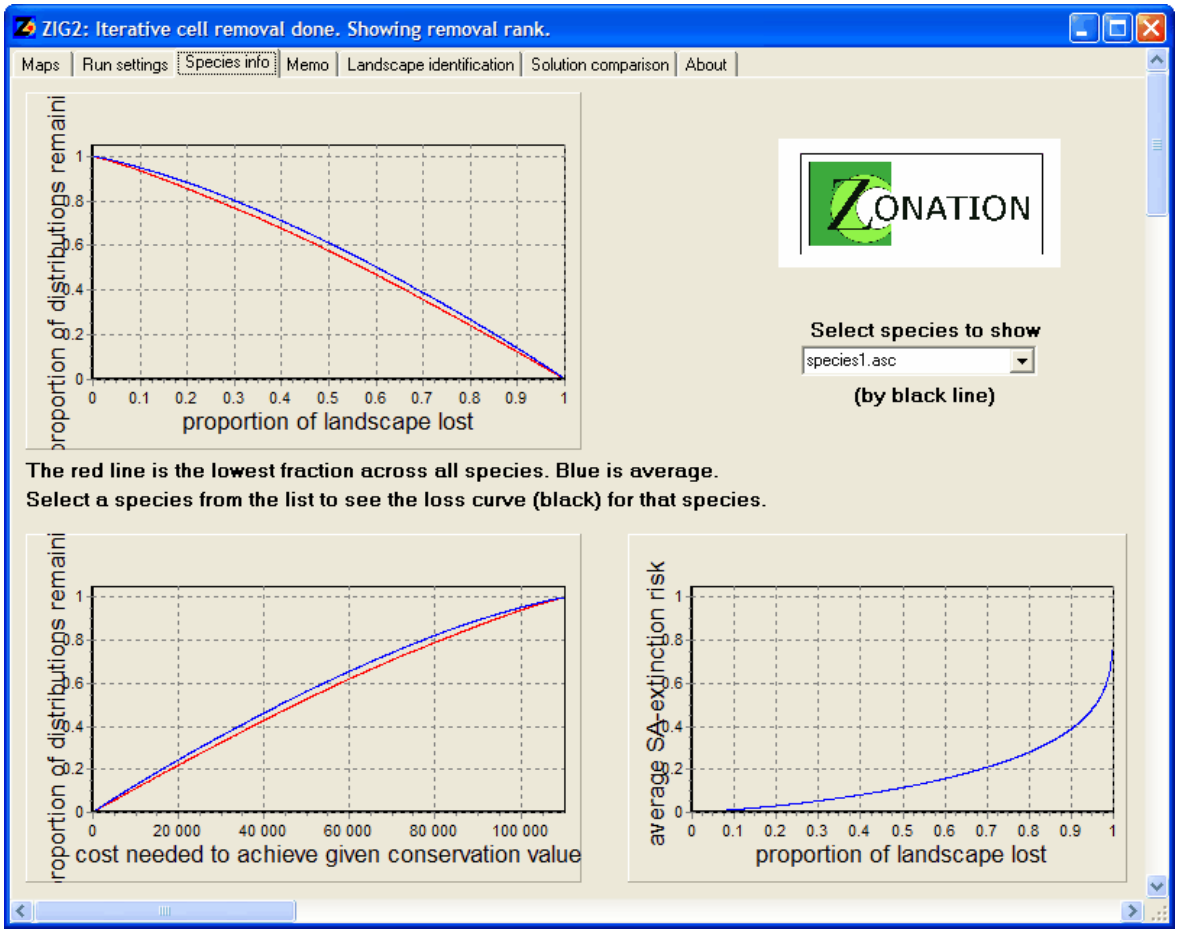
7. **Wmap.** If you are including uncertainty in species distribution in to your analysis, this option shows you how the uncertainty of your data is distributed in the landscape for the species you select.

Species info -window

In the "Species info" -window you can see three curves, the first of which shows the **proportion of distribution remaining** for each species when landscape is removed. The red line represents the species with the lowest distribution remaining, and the blue line represents the average over all species. You can select from the dialog box a respective curve for each species, which is shown in black. Note that this species line can be hidden under the main lines! Below the distribution curve is the **cost curve** showing how high costs are needed for buying the respective top fraction. If no cost layer is used, all cells receive an equal value of 1.0 and the curve thus show the number of cells

© 2004-2006 Atte Moilanen

needed for respective top fractions. The curves begin from the proportion of landscape that is left after the initial removal of the worst proportion. If nothing is removed, the curve starts from zero, as below. The third curve shows how the extinction risk of species increases as landscape is removed. This curve is based on the species-area ratio and shows the average extinction risk over all species.

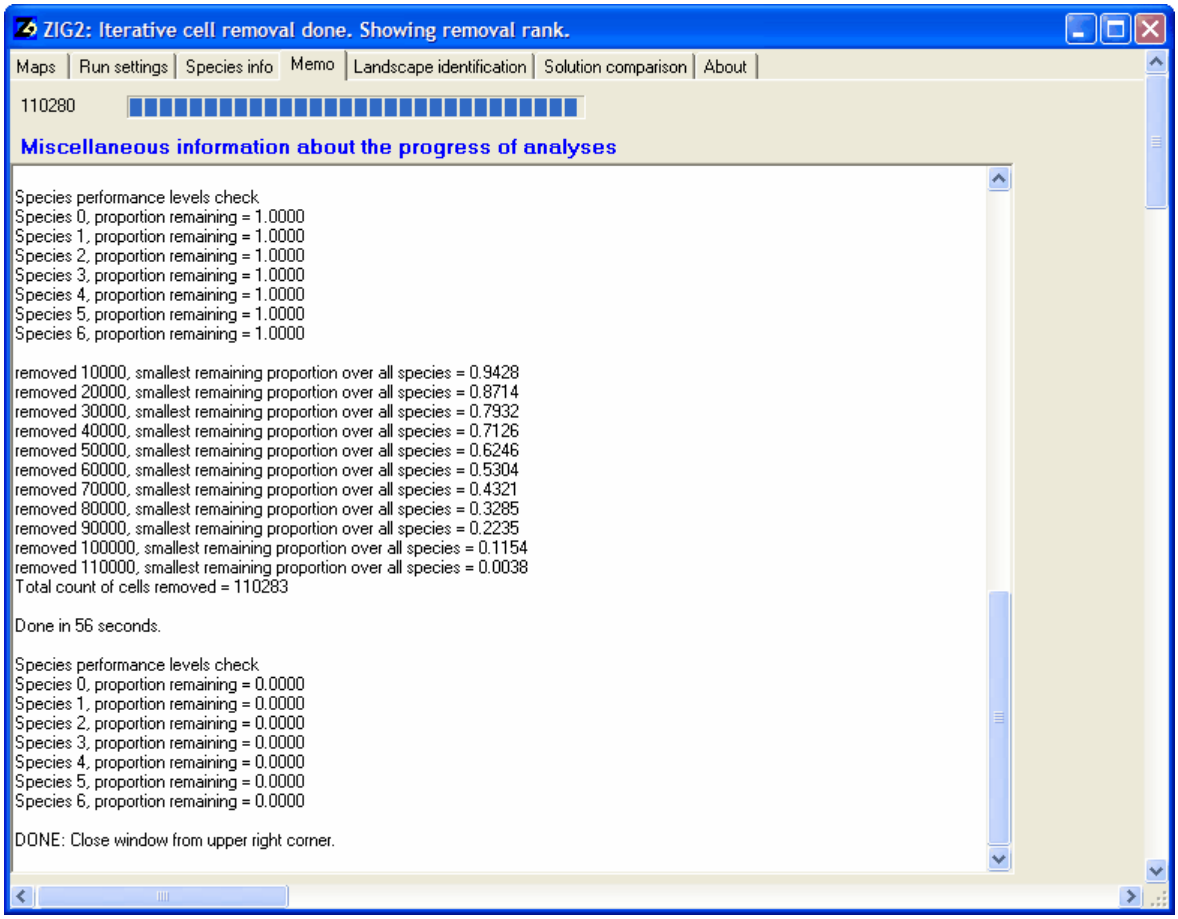

ZIG2: Iterative cell removal done. Showing removal rank.
Maps
Run settings
Species info
Memo
Landscape identification
Solution comparison
About
proportion of distributions remaini
proportion of landscape lost
ZONATION
Select species to show
species1.asc
(by black line)
The red line is the lowest fraction across all species. Blue is average.
Select a species from the list to see the loss curve (black) for that species.
proportion of distributions remaini
cost needed to achieve given conservation value
average SA-extinction risk
proportion of landscape lost

Picture of the "Species info" -window.

© 2004-2006 Atte Moilanen

Memo -window

The Memo keeps track of what the program is doing or has been doing.


ZIG2: Iterative cell removal done. Showing removal rank.
Maps
Run settings
Species info
Memo
Landscape identification
Solution comparison
About
110280
Miscellaneous information about the progress of analyses
Species performance levels check
Species 0, proportion remaining = 1.0000
Species 1, proportion remaining = 1.0000
Species 2, proportion remaining = 1.0000
Species 3, proportion remaining = 1.0000
Species 4, proportion remaining = 1.0000
Species 5, proportion remaining = 1.0000
Species 6, proportion remaining = 1.0000
removed 10000, smallest remaining proportion over all species = 0.9428
removed 20000, smallest remaining proportion over all species = 0.8714
removed 30000, smallest remaining proportion over all species = 0.7932
removed 40000, smallest remaining proportion over all species = 0.7126
removed 50000, smallest remaining proportion over all species = 0.6246
removed 60000, smallest remaining proportion over all species = 0.5304
removed 70000, smallest remaining proportion over all species = 0.4321
removed 80000, smallest remaining proportion over all species = 0.3285
removed 90000, smallest remaining proportion over all species = 0.2235
removed 100000, smallest remaining proportion over all species = 0.1154
removed 110000, smallest remaining proportion over all species = 0.0038
Total count of cells removed = 110283
Done in 56 seconds.
Species performance levels check
Species 0, proportion remaining = 0.0000
Species 1, proportion remaining = 0.0000
Species 2, proportion remaining = 0.0000
Species 3, proportion remaining = 0.0000
Species 4, proportion remaining = 0.0000
Species 5, proportion remaining = 0.0000
Species 6, proportion remaining = 0.0000
DONE: Close window from upper right corner.
Picture of "Memo" -window.

3.4.2 Automated file output

In addition to the visual output, the program automatically produces six different output files for each run. In the command line, or in the windows versions' "Run settings" -window you have specified the output filename, e.g. "output", which will be used for each of the output files with a varying suffix: output.jpg, output.emf, output.curves.txt, output.prop.asc, output.rank.asc and output.run_info.

.jpg file

An image of the map of the area illustrating the Zonation results, ranked by using different colours to indicate the biological value of the site. Here the best areas are displayed in red and the worst areas in black, with the "no data" -areas marked as white. See section 3.4.1 Visual output for more detailed interpretation of the colours used in landscape ranking.

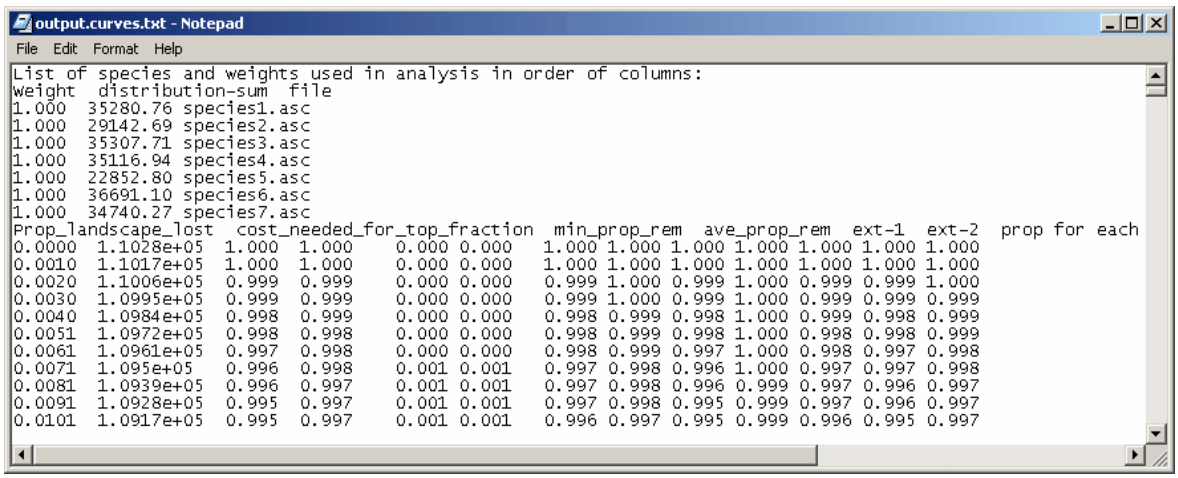
.emf file

This is an identical image showing your output map, but it has a higher quality compared to the .jpg file. Thus, if you are using any of the images in publications, it is recommended to use this file type.

© 2004-2006 Atte Moilanen

.curves.txt file

A text file containing a list of species and the relative weights used in the analysis, together with the initial sum of species distributions. The initial sum of distribution is simply the sum of each species values in landscape. E.g., if your species data is in probabilities of occurrence, this is the sum of probabilities in all cells before any landscape has been removed. After the list you can find columns representing how large proportion of distribution of each species is remaining when landscape is iteratively removed.

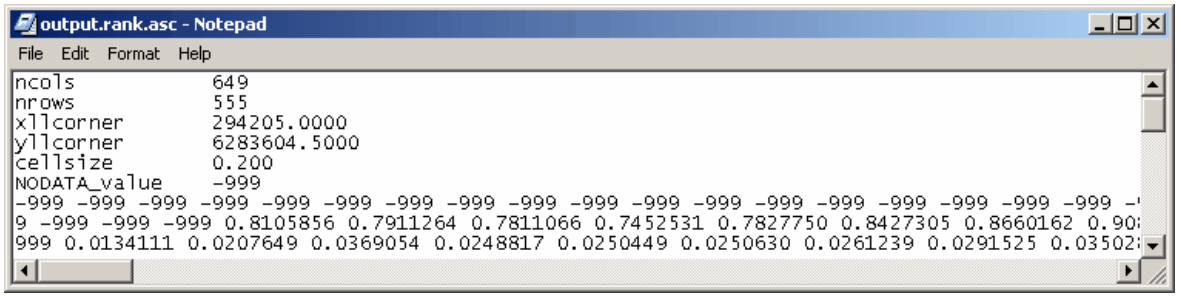


Picture of output.curves.txt file.

The first column gives the proportion of the landscape removed. If you have initially removed some parts of the landscape before running the program (initial removal), the file contains only those areas that are included in the analysis. **The second column** shows the cost of remaining landscape. If land costs are not included in the analysis, this column represents the number of cells that is remaining in the landscape. **The third column** shows the minimum proportion of species distribution that is remaining in the landscape, thus the situation of the worst-off species. **The fourth column** represents the average proportion over all species. **The fifth column** shows the average extinction risk of species as landscape is iteratively removed (as calculated from the species-area relation) and **the sixth column** is the weighted extinction risk where species-area extinction risk has been weighted by the species weights. **The following columns** show the proportion of distribution remaining for each species in the same order as the species are listed in the beginning of the file. Note, that for the output file to be readable, the program does not print every step of cell removal (this file only includes a maximum of 10 000 rows).

.rank.asc file

A raster file representing the ranking of the landscape, or in other words, the order of cell removal. The file includes all basic raster information as explained in species distribution map files and a matrix of cell removal order. Here the cells receive a value between 0 and 1. Low values close to zero indicate that the cell has been removed in a early state of the process whereas cells with high value are removed last.



Picture of ouput.rank.asc file.

© 2004-2006 Atte Moilanen

.prop.asc file

A raster file similar to .rank.asc -file. Here, however, the matrix shows the proportional loss of distribution for that species, that has lost most of its distribution during the landscape removal process. E.g. if a cell has a value of 0.7, it means that after removing that cell all species have at least 30 % of their distribution left (the value 0.7 indicates that one of the species, which is doing worst after removing that particular cell, has lost exactly 70 % of its distribution).

Useful information

.rank.asc and **.prop.asc.** files are raster files, which can be used to produce map images in GIS software. For example, in ArcView choose "Import Data Source..." from "File" -options and select ASCII raster as your import file type. Select the file you wish to import, rename it and **do NOT choose integer cell values**.
The rank-file is the one that can be loaded with the -l -command, and that can be used in landscape comparison (see section 3.6.3).

.run_info file

A text file copy of the Memo. This file will be created only after you have closed the program. You can use it to go back to see what happened in your analyses. Note that some error messages or warnings may appear here.

3.5 Main analyses

3.5.1 Basic Zonation and species weighting

The basic Zonation run ranks the cells in a landscape based on their conservation value. The theory and algorithm behind basic Zonation is explained in sections 2.2 and 2.3.

Running basic Zonation

For running the basic Zonation, you need to have all the compulsory input files:

1. Species distribution files, one file per each species
2. Species list file
3. Run settings file (only when operating the program from the command prompt!)

You can run the program either from the command prompt or from the windows interface. Note that as with any other analysis, you can also write a batch file and use it to run the program.

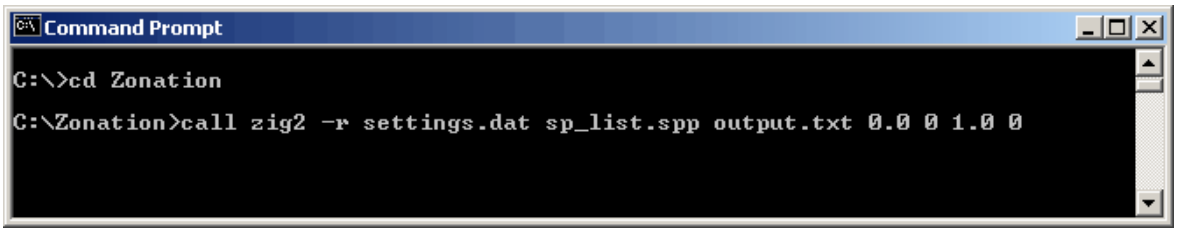
In the command prompt

1. Set all options of **additional analyses** (e.g. BQP, uncertainty analysis etc.) to zero in your **run settings file** AND in the **command prompt call** to indicate that no additional analyses are used.
2. Adjust your settings in the run settings file for the following options if necessary:
   - warp factor
   - edge removal
   - add edge points
   - logit space

   Note that if you do NOT select the edge removal, the computation times will increase significantly with large data sets.
3. Adjust the species weights in **species list file** if you wish to stress the conservation of certain species (e.g. rare species of high conservation value or commercially valuable species).
4. Type the call for Zonation in the command prompt and press enter to initiate the computation.

See section 3.2.1 for how to use the command prompt.

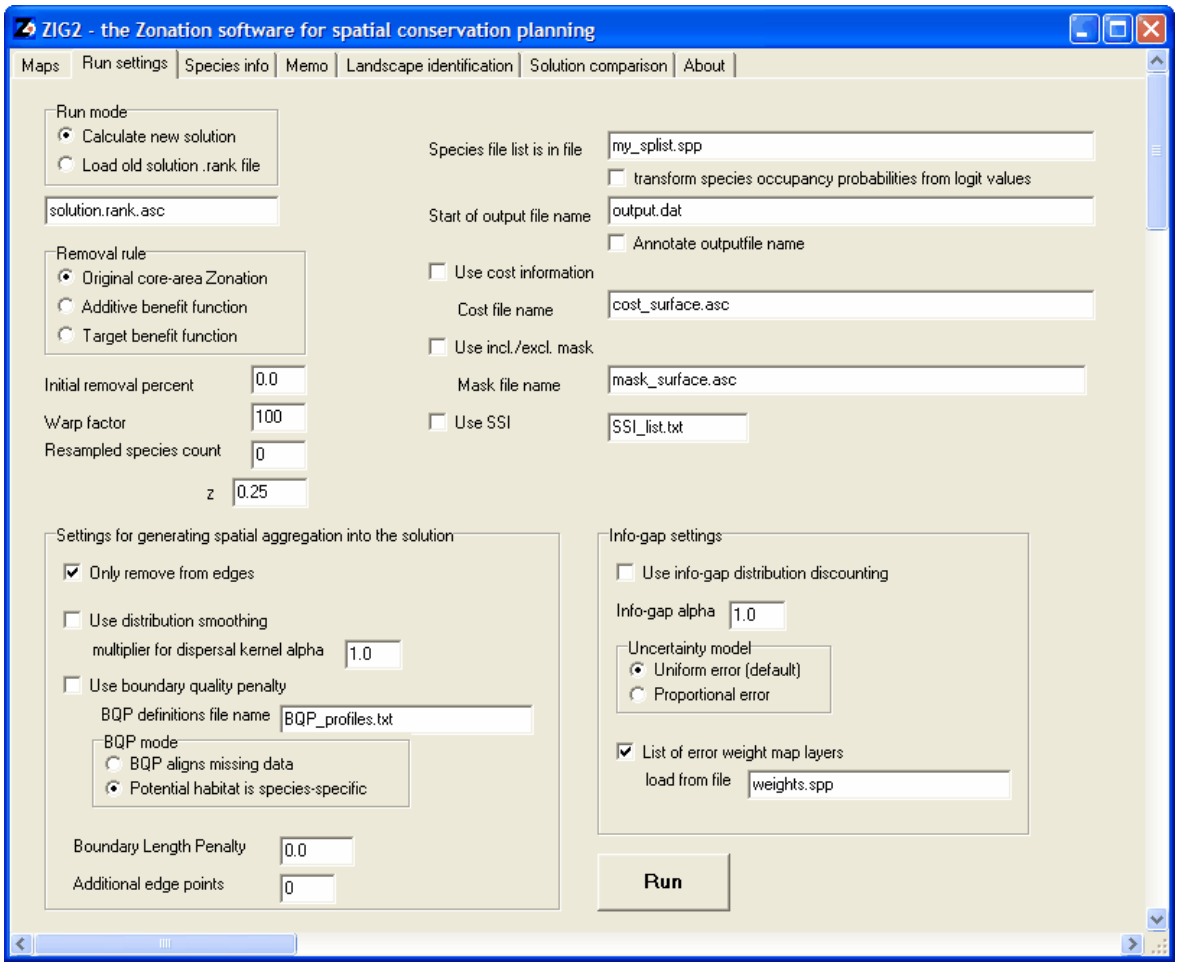
© 2004-2006 Atte Moilanen



Picture of basic Zonation call.

In the windows interface

1. Go to **Run settings -window** and check that no additional analyses are selected.
2. Adjust the settings as described in command prompt above.
3. Adjust the species weights in **species list file** if you wish to prioritize certain species.
4. Define the names of your species list file and output file and press "Run" to initiate the computation.



Picture of Run settings -window when running basic Zonation without any additional analyses.

Weighting of species is a critical component of the algorithm. Problems associated with different initial sizes of species distributions are circumvented in Zonation by assigning a value for the full distribution of each species. By default, these values are equal, but species can be assigned differential weights (in the **species list file**) based on, for example, their taxonomic status, global rarity, economical value or population trend. Weighting of species affects the order in which cells are removed from the landscape. Cells that include a part of the distribution of a valuable species (high weight) remain later in the iterative cell removal process than cells only containing low-weight species, assuming everything else is equal between the occurrences. Weighting influences the fraction of a species distribution retained at any point of the cell removal. If species have equal weights, approximately equal fractions are retained irrespective of differences in the absolute sizes of the original full distributions. When using weighting, high-weight species retain a relatively higher

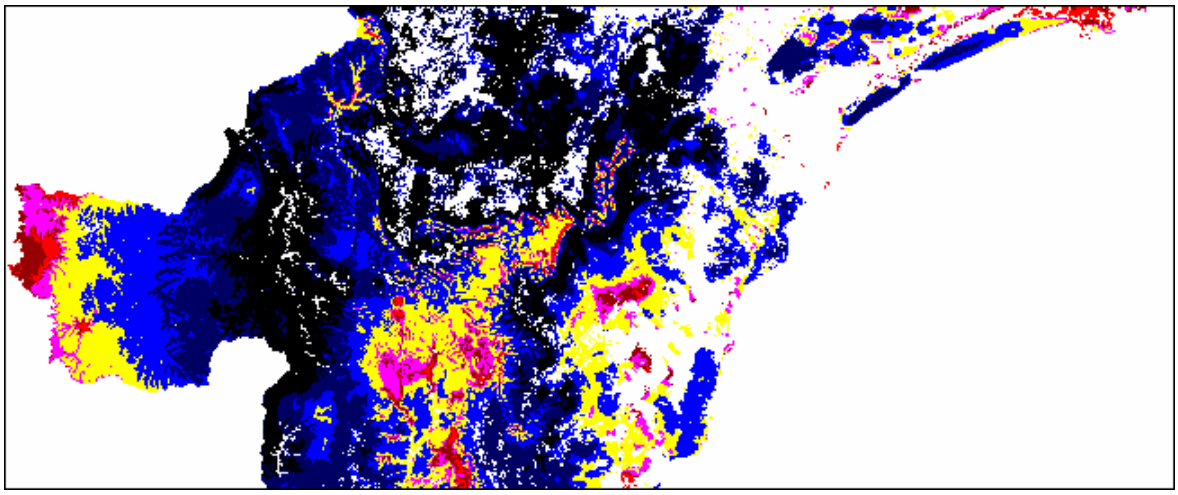
© 2004-2006 Atte Moilanen

proportion of their distribution.

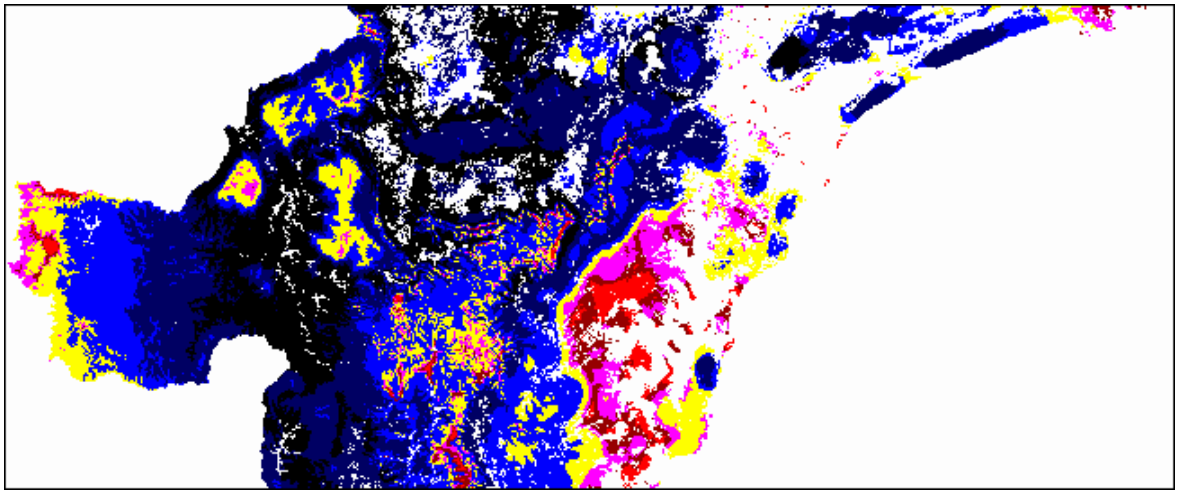
Note that weights can also be used to test the efficiency of **surrogate species**. This is done by weighting the surrogate species normally (e.g. by 1) and giving a weight of 0 to all those species that are NOT used as surrogates. This way the program will not use the non-surrogate species in the selection of the next site to remove, but it will monitor the decrease of the distributions of these species as well. Thus, you can test how well a reserve network selected using surrogates will protect all species.

Output

Here is an example of how species weighting can influence the final solution. The pictures show the results of two basic Zonation runs for seven species. In the first picture no species weights have been used where as in the second picture one of the species has received a weight of 3.0.



Picture of solution when no weights are used.



Picture of solution when one of the species has a weight of 3.0.

3.5.2 Distribution smoothing + Zonation

Distribution smoothing is a two-dimensional kernel smoothing, where the width of the smoothing kernel is determined by the estimated dispersal ability or scale of landscape use of the species in question. This option results a much more compact solution, where small isolated patches have been removed. Using distribution smoothing increases computation times marginally if at all. The theory and algorithm behind distribution smoothing is explained in section 2.4.1. This method is also described in Moilanen *et al. (*2005) *Proc. R. Soc. B* **272**: 1886 →, and Moilanen & Wintle

© 2004-2006 Atte Moilanen

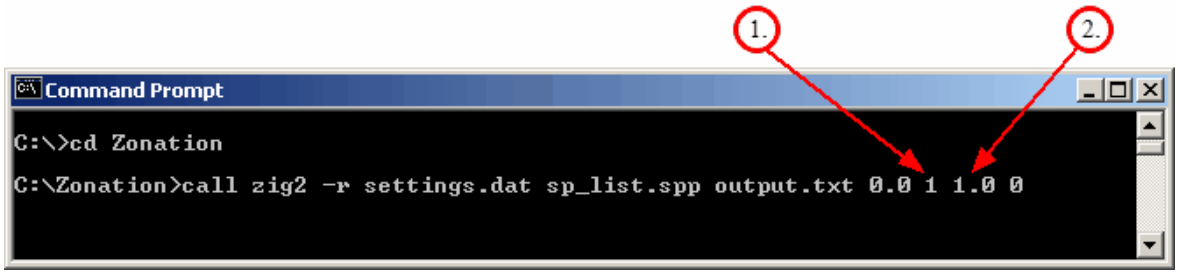
(2006) *Biol. Conserv.* **129:** 427-434.

Running distribution smoothing

To get distribution smoothing done you need to:

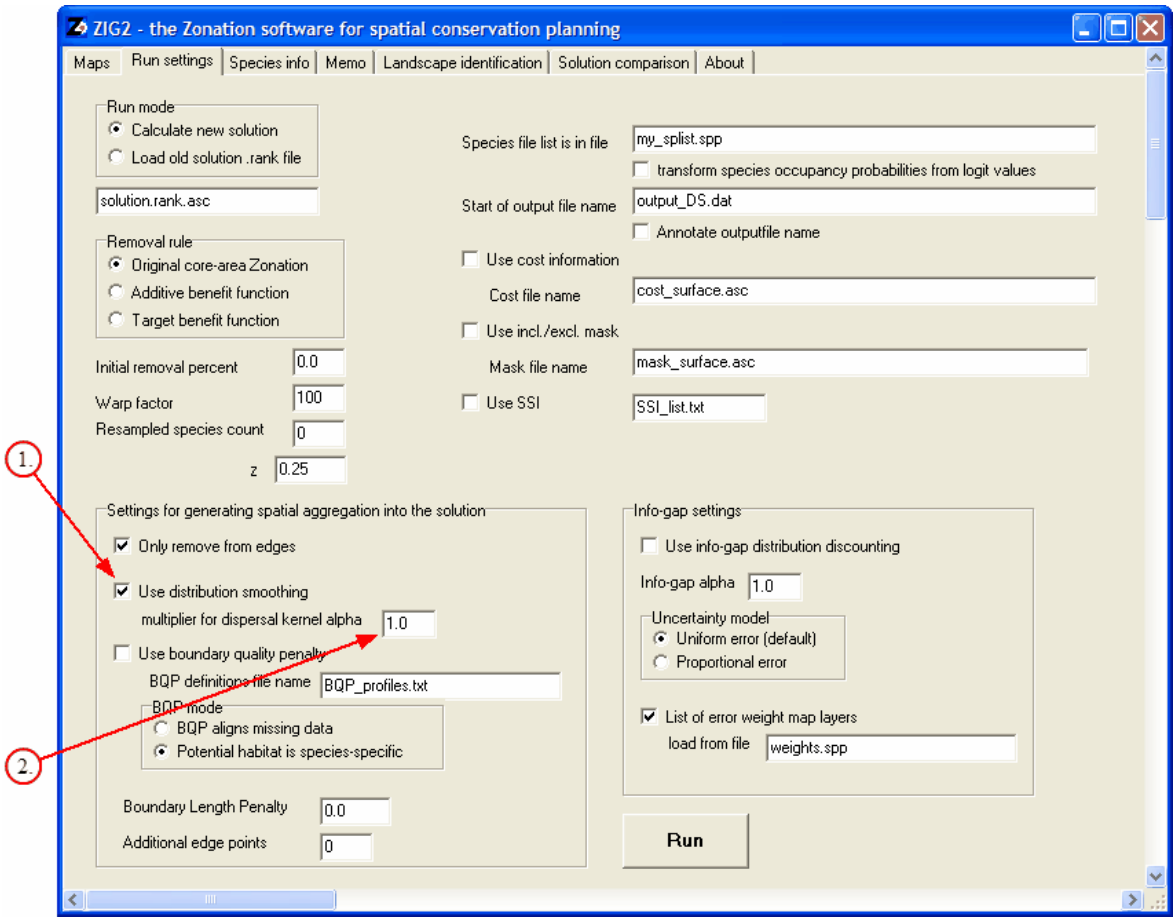
In the command prompt

1. Set the third last parameter of your call to 1 to indicate that distribution smoothing will be done.
2. Give a factor for multiplying the **species-specific** α **-values** as the second last parameter in your call. α -values (species-specific widths of kernel) are in the second column of your species list file. The factor is useful if you are interested in running multiple solutions with, e.g. assuming several levels of dispersal capabilities, because the factor allows you to multiply all dispersal capabilities simultaneously. Thus you do not need to change the parameters manually in the species list file after each run. If you do not wish to multiply the α -values, set this factor to 1.



In the windows interface

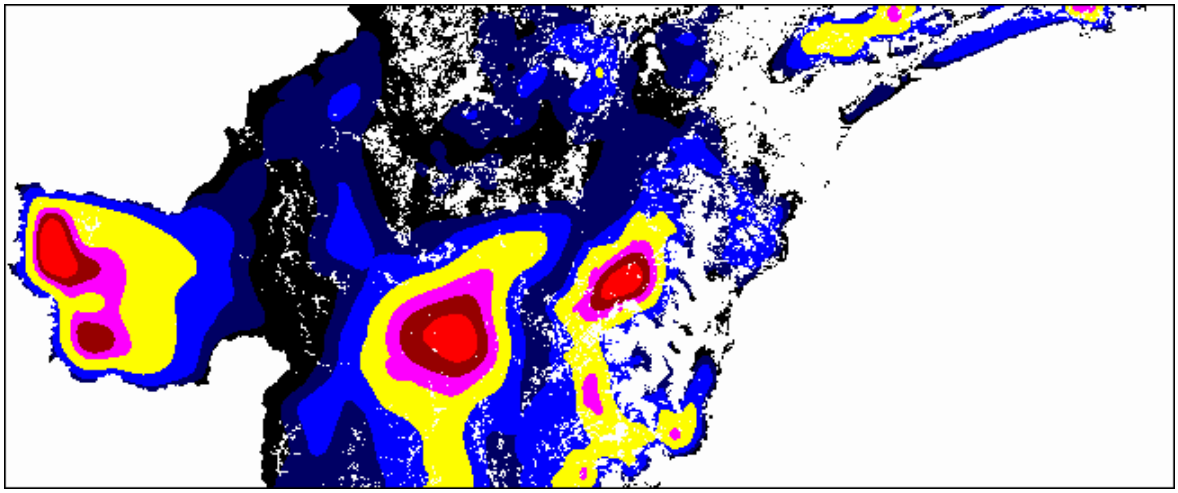
1. Select the distribution smoothing option
2. Give a factor for multiplying the species-specific α -values.



© 2004-2006 Atte Moilanen

Output

Note that using distribution smoothing should result a distinctively more aggregated solution compared to basic Zonation analysis. Thus these two solution should probably not have, e.g., a 99% overlap with each other. If your solution with distribution smoothing does not show clear aggregation, check the run settings for possible errors: for example, you could have α in different units than the cell size in the species distribution files. See section 3.8 for trouble shooting.



Picture of a typical output map when distribution smoothing has been included in the analysis.

3.5.3 BQP Zonation

The boundary quality penalty (BQP) is a quantitative method that induces aggregation into reserve networks according to the needs of individual species. Using the BQP decreases the biological quality of a land unit (grid cell) that is located close to the edge of the reserve, which results in a more highly aggregated optimal reserve structure. The theory and algorithm behind boundary quality penalty is explained in section 2.4.2. This method has also been described in Moilanen & Wintle 2007 (*Conserv. Biol.*, in press).

Running BQP

To include BQP in to your analysis you need to:

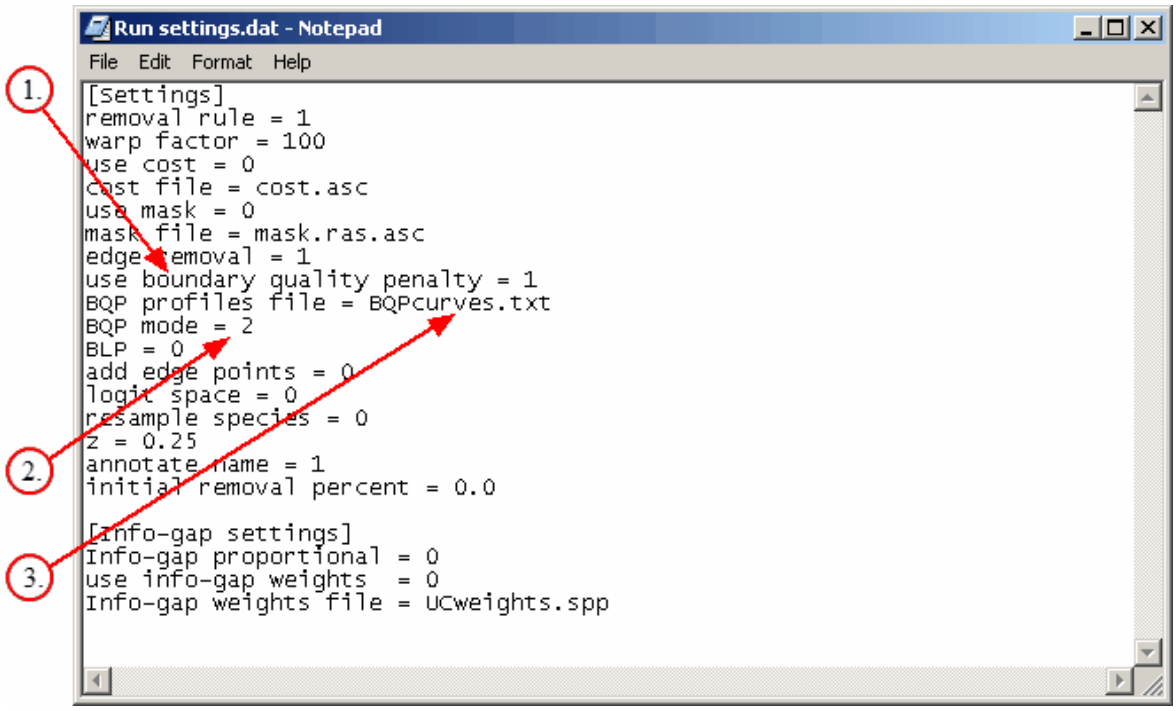
1. Create a BQP definition file which contains all penalty curves. This file determines different responses of species to habitat fragmentation.
2. Link all species to the correct penalty curve by entering the correct row number of the respective curve into the third column of your species list file.
3. Give a suitable buffer size (in cells!) for each species in your species list file. The buffer size indicates the area in which any habitat loss and fragmentation will influence the biological value of the focal cell.

In addition you need to adjust your settings:

In the command prompt

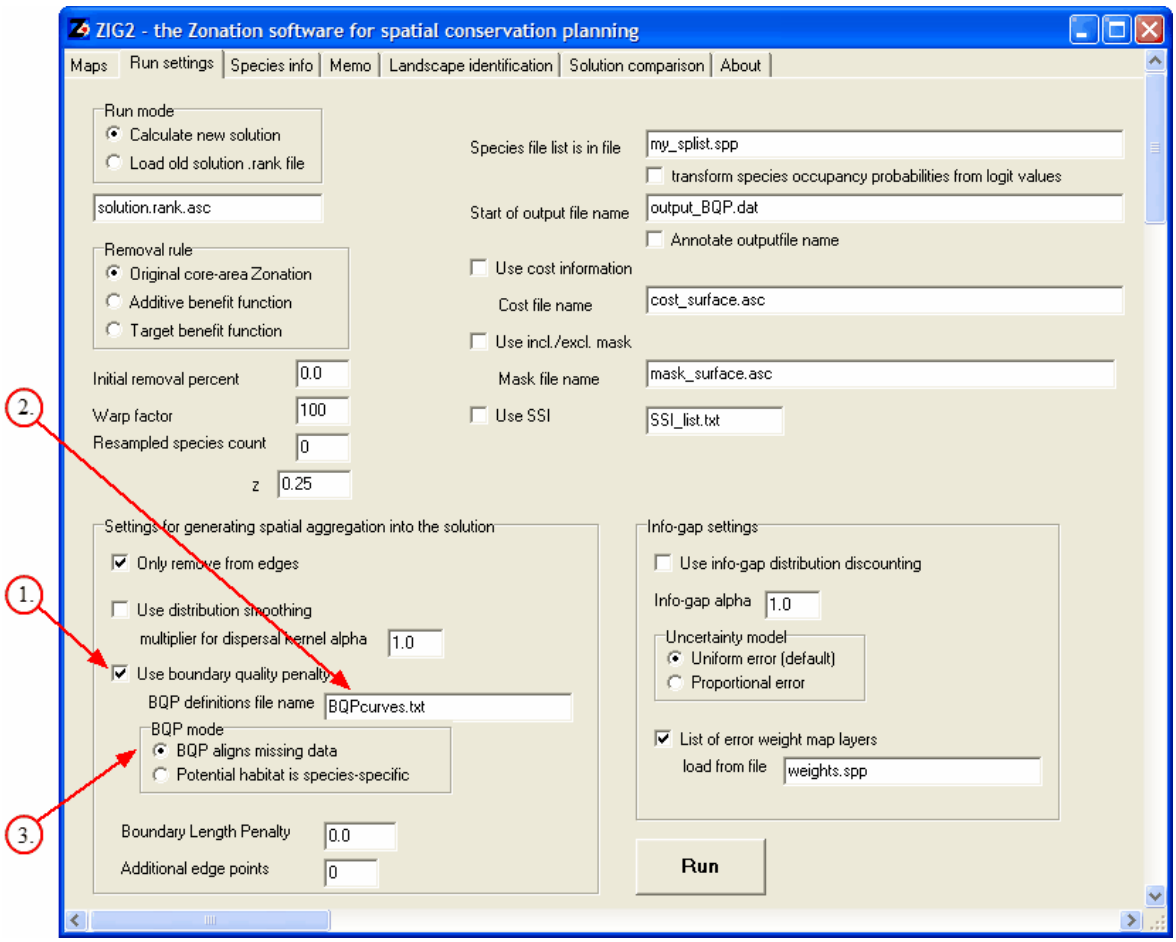
1. Set "`use boundary quality penalty`" to 1 in your run settings file to indicate, that BQP will be used.
2. Also define the name of your BQP definition file in the run settings file.
3. Select the correct BQP mode based on whether the data/no data matrix of your species distribution layers is uniform in all layers or if there are differences between the layers.

© 2004-2006 Atte Moilanen



Note that you do not need to make any changes to the actual call in command prompt for using BQP.

In the windows interface

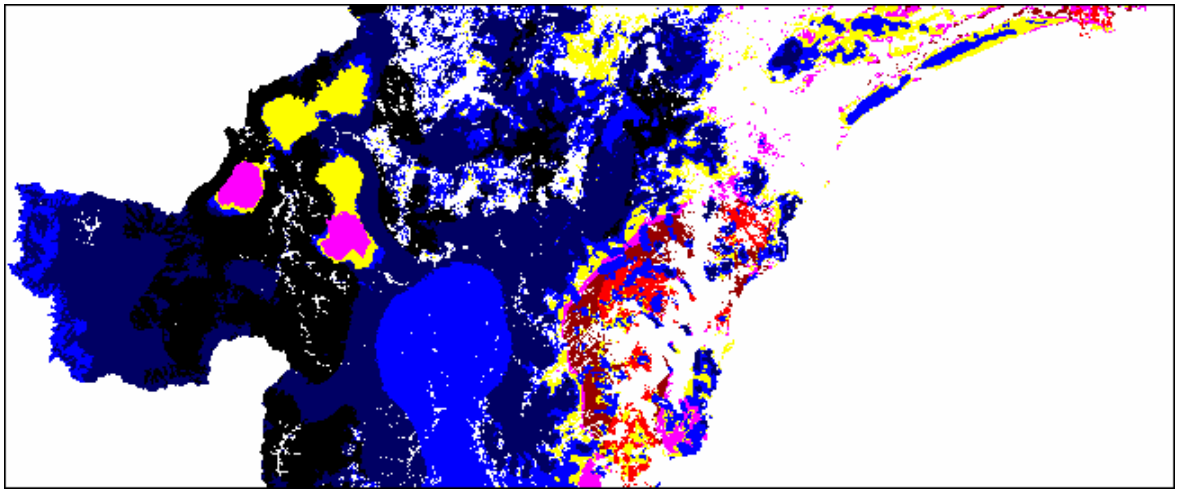


© 2004-2006 Atte Moilanen

1. Select the BQP option from the **Run settings -window**.
2. Define the name of your BQP definition file.
3. Select the correct BQP mode based on whether the data/no data matrix of your species distribution layers is uniform in all layers or if there are differences between the layers.

Output

Including BQP into your analyses most likely increases computation times significantly, especially if the species-specific buffer sizes are large (many cells). Thus it might be wise to reduce the data resolution if computation times start to increase in undesirable ways. It is also recommended to use a high warp factor for your preliminary runs and a low warp factor only for making the final solutions. Using BQP should result in a distinctively more aggregated solution compared to basic Zonation analysis, at least in some part of the landscape. Thus, these two solutions should not have, e.g. 99% overlap with each other, unless your species are not influenced by habitat loss (as defined in the BQP file). If your solution with BQP shows signs of high fragmentation, check the run settings for possible errors. Note however, that a BQP solution may well include fragmented areas, if the data contains many species that are indifferent to fragmentation or even favor fragmented habitats.



Picture of typical output map when BQP has been included in the analysis.

3.5.4 Including distributional uncertainty - Distribution discounting

Distribution discounting is a method to include uncertainty analysis (UCA) to reserve selection process. With distribution discounting you can compare the performances of different solutions as uncertainty increases. Essentially this method seeks a solution that has high robustness in achieving a given conservational target despite the uncertainty. The theory and algorithm behind distribution discounting is explained in section 2.5.1. This method is also described in Moilanen *et al.* (2006), *Conserv. Biol.* **20**: 1688-1697.

Running distribution discounting

To include distribution uncertainty in your analysis you first need to define the scale of uncertainty. As explained in section 2.5.1, this can be done by giving values to (1) the uncertainty parameter α and (2) to the species- and cell-specific relative error measure $\boldsymbol{w_{sc}}$. Species-cell-specific relative errors are the ones given in the uncertainty map layers. **Using species-cell-specific errors (i.e. the uncertainty map layers) is optional, but you always have to give a value to the uncertainty parameter**.

Note that if you are using α as the only measure of error (thus not using the distributional uncertainty map layers), it is important that the value of α is determined in relation to your data. For example, if your species data are probabilities of occurrence [0,1], the uncertainty parameter should

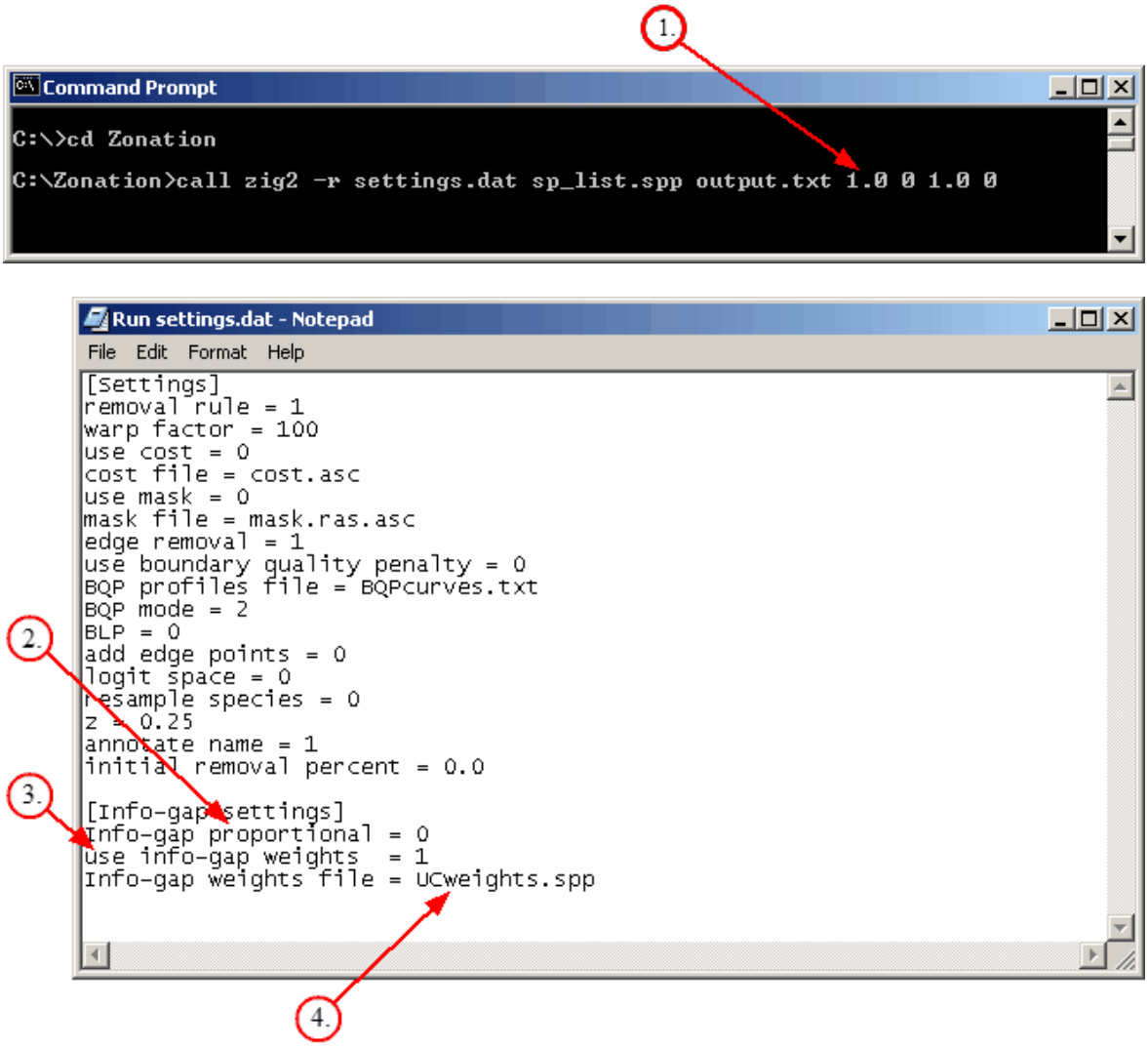
© 2004-2006 Atte Moilanen

be set to a reasonably small scale (e.g. $\alpha < 0.4$) to avoid complications, which may arise if all cells receive an effective discounted value of zero.

1. Distribution uncertainty map layers for each species. These layers show the relative magnitude of error (uncertainty) of species occurrence in each cell. Remember that the meaning of α must be interpreted with respect to the error measure you use. For example, if your error measure is the standard error of statistical prediction, then α=1 essentially means subtracting one SD from the value of each cell.
2. Uncertainty analysis weights file containing a list of each distribution uncertainty layers and species-specific **error weights**. With error weights you can stress the data accuracy for certain, e.g. very rare, species. If no species uncertainty analysis weights are used, these parameters should be set to 1.0. Note that you can not use species-specific error weights without the distribution uncertainty map layers.

In addition you need to adjust your settings and the program call in the command prompt:

In the command prompt



1. Give a value to the uncertainty parameter α in your program call (the fourth last parameter). α -value determines the horizon of uncertainty in the data and is usually unknown. Thus you need to test generate solutions with several α -values to determine how the spatial pattern behaves with increasing uncertainty. α can be either zero (= no uncertainty) or any positive value.
2. Define in the run settings file whether errors in species occurrences are uniform (value = 0) or proportional (value = 1). Uniform error is the default setting and works for most of the data sets, but in some cases it is more appropriate to use proportional errors (see e.g.

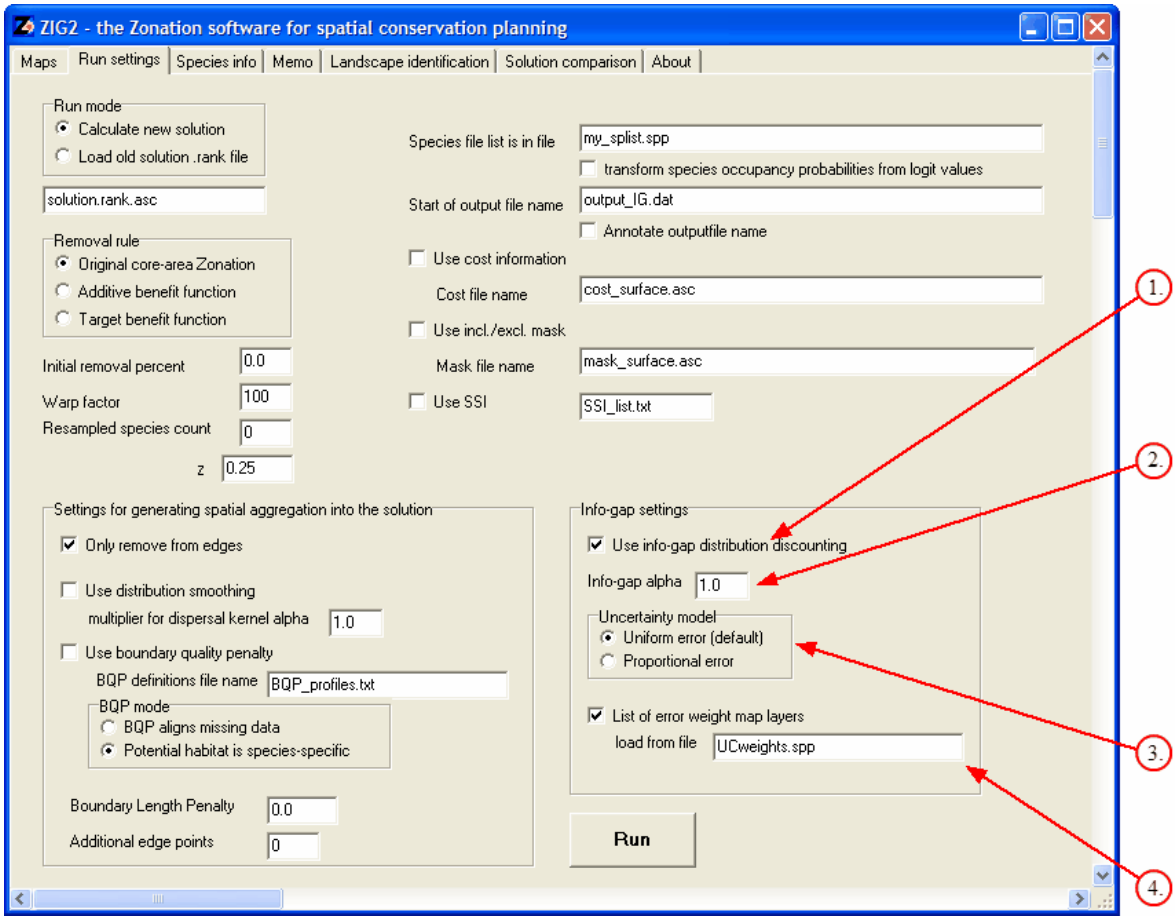
© 2004-2006 Atte Moilanen

Ben-Haim 2001).

3. Define whether uncertainty map layers (containing species-cell-specific errors w_{sc}) are used (value = 1) or not (value = 0) in your run settings file.
4. If distribution uncertainty map layers are used, type the name of your uncertainty analysis weights file in to the run settings file. E.g. "`Info-gap weights file = UCweights.spp`".

In the windows interface

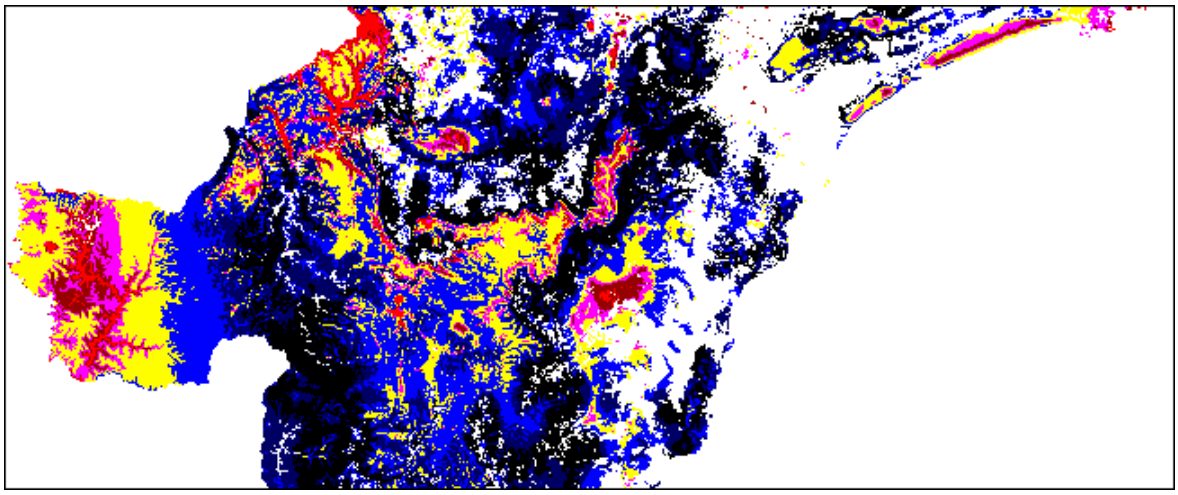
1. Select the distribution discounting option.
2. Give a value to the uncertainty parameter α.
3. Select whether you wish to use uniform or proportional errors.
4. Select the "List of error weight map layers" -option and give the name of your uncertainty analysis weights file, if you wish to include the uncertainty map layers into the analysis.



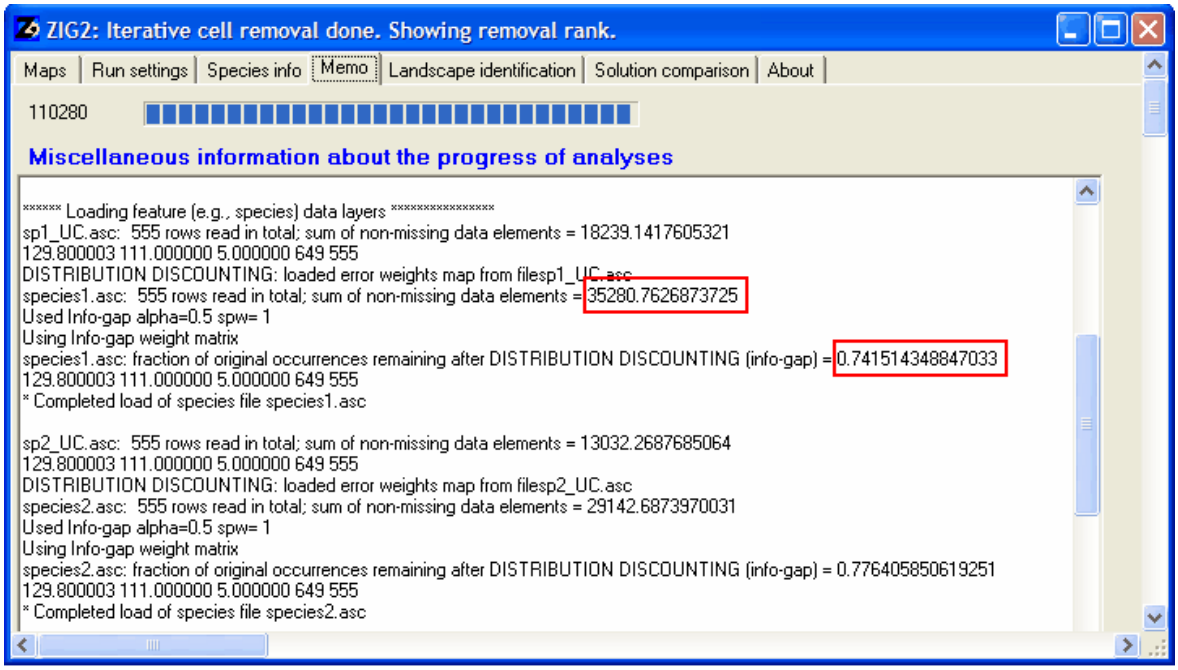
Output

The analysis produces a standard map of the landscape where reddish colours indicate sites that have both high species occurrence and high certainty. Depending on the amount of error in your data, the differences between the basic Zonation solution and distribution discounting can be significant - or not. In the Memo -window you can find more detailed information about the analysis. Note that as the program starts to run the analysis, it recalculates the species values based on the amount of uncertainty. Thus, for each species, the program first displays the absolute value in the whole landscape (sum over all cells) and then calculates how large fraction of this value can be expected to occur in the landscape with certainty. This value depends on the horizon of uncertainty parameter and on the level of uncertainty in the data.

© 2004-2006 Atte Moilanen



Picture of our example landscape when uncertainty in species occurrences is included in the analysis.


ZIG2: Iterative cell removal done. Showing removal rank.
Maps
Run settings
Species info
Memo
Landscape identification
Solution comparison
About
110280
Miscellaneous information about the progress of analyses
****** Loading feature (e.g., species) data layers **********
sp1_UC.asc: 555 rows read in total; sum of non-missing data elements = 18239.1417605321
129.800003 111.000000 5.000000 649 555
DISTRIBUTION DISCOUNTING: loaded error weights map from filesp1_UC.asc
species1.asc: 555 rows read in total; sum of non-missing data elements = 35280.7626873725
Used Info-gap alpha=0.5 spw= 1
Using Info-gap weight matrix
species1.asc: fraction of original occurrences remaining after DISTRIBUTION DISCOUNTING (info-gap) = 0.741514348847033
129.800003 111.000000 5.000000 649 555
* Completed load of species file species1.asc
sp2_UC.asc: 555 rows read in total; sum of non-missing data elements = 13032.2687685064
129.800003 111.000000 5.000000 649 555
DISTRIBUTION DISCOUNTING: loaded error weights map from filesp2_UC.asc
species2.asc: 555 rows read in total; sum of non-missing data elements = 29142.6873970031
Used Info-gap alpha=0.5 spw= 1
Using Info-gap weight matrix
species2.asc: fraction of original occurrences remaining after DISTRIBUTION DISCOUNTING (info-gap) = 0.776405850619251
129.800003 111.000000 5.000000 649 555
* Completed load of species file species2.asc

Picture of the Memo -window when running distribution discounting.

3.5.5 Inclusion/Exclusion cost analyses using mask files

This is a method that allows you to include or exclude specific areas to or from the final reserve design, and to evaluate the following costs of using a possibly suboptimal solution. The theory behind the replacement cost analysis is explained in section 2.6. To find out more about replacement cost analyses, see Cabeza & Moilanen (2006) *Biol. Conserv.* **132**: 336-342.

Running the analysis with a mask file

To include/exclude areas to/from the final solution you need a

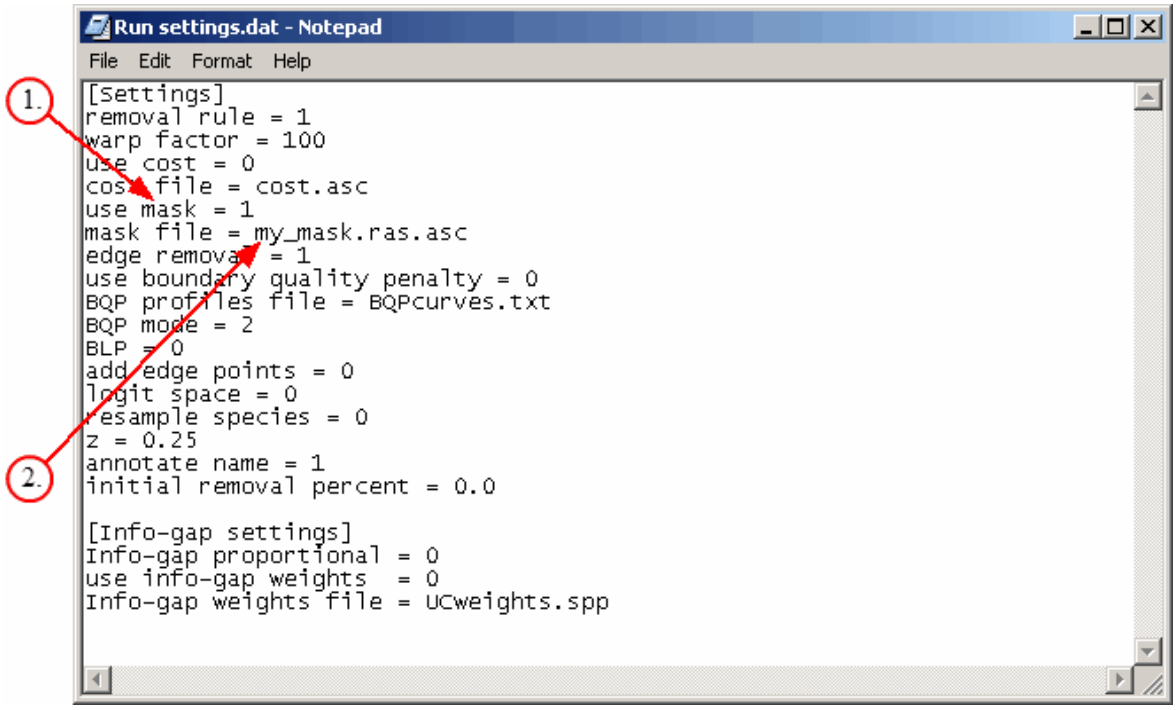
1. Removal mask file in which the hierarchy of cell removal is determined. This file tells the program if some areas need to be included to the top fraction (e.g. old reserves) or excluded from it (e.g. areas ear-marked for residential building).

In addition you need to adjust your settings:

© 2004-2006 Atte Moilanen

In the command prompt

1. Set "`use mask`" to 1 in your settings file to indicate that a removal mask is used.
2. Give the name of your removal mask file.

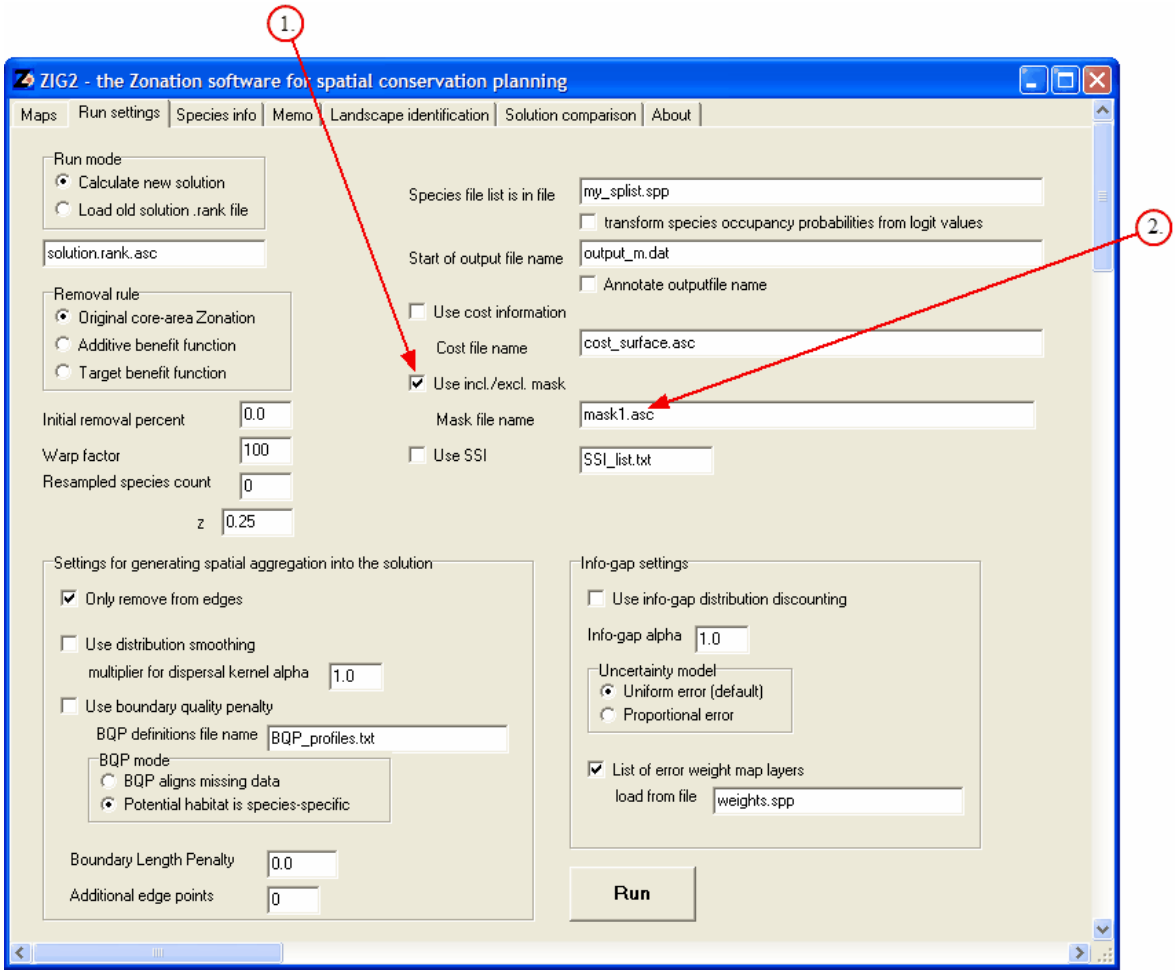


Note that you do not need to make any changes to the actual call in the command prompt for using a mask file.

In the windows interface

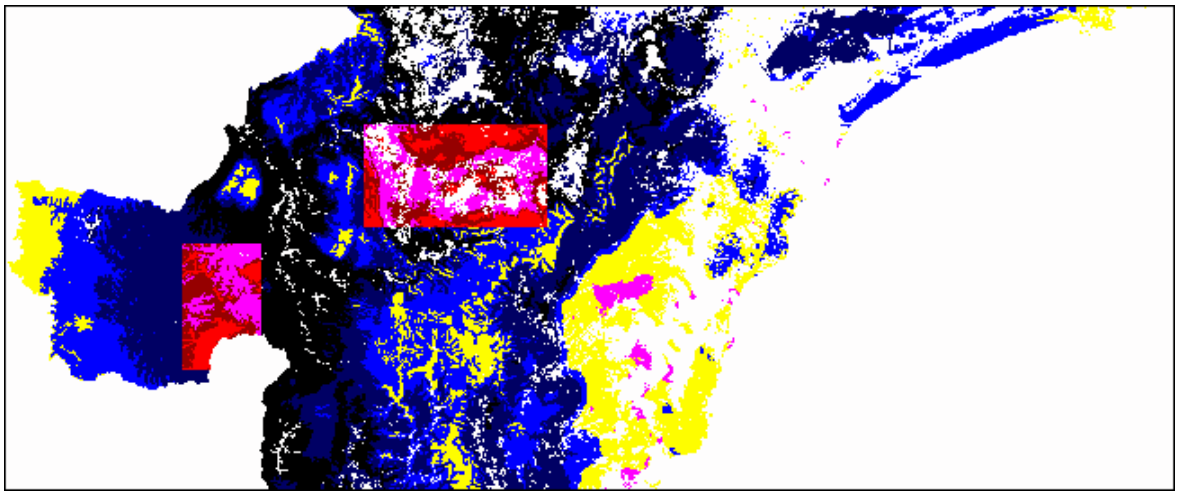
1. Select the "Use incl./excl. mask" -option from the **Run settings -window**.
2. Define the name of your removal mask file.

© 2004-2006 Atte Moilanen



Output

The effects of running the analysis with a mask file should be clearly seen from your output map. The included areas should receive the highest values in landscape ranking where as the excluded areas receive the lowest values.

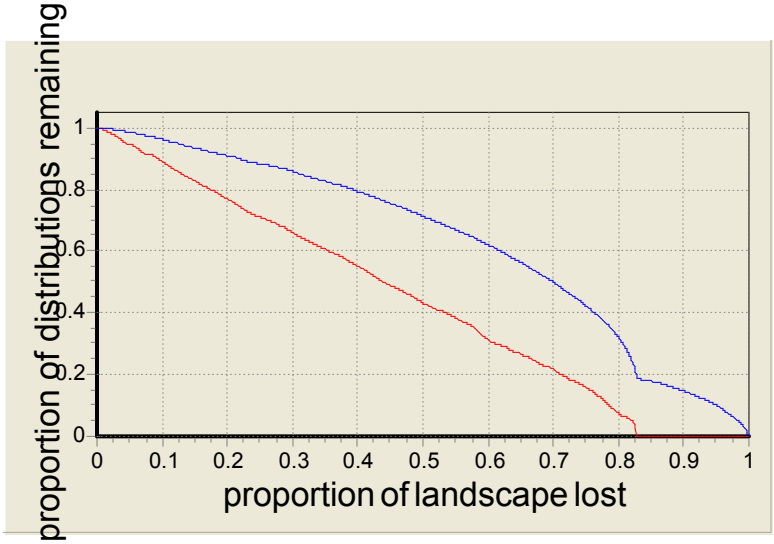


Picture of our example landscape when two large areas have been forcibly included to the final solution with a mask file.

Also the distribution curves in **Species info -window** may show some changes depending on the

© 2004-2006 Atte Moilanen

areas that have been included/excluded. Note that in many cases the use of mask files results a suboptimal solution. In other words, the program cannot select the best possible solution, because it is forced to either exclude biologically valuable areas from or include poor quality areas into the top fraction.



Picture of distribution curves when the program has been forced to include low quality areas to the solution. Note the changes at the end of the curves.

By comparing the .curves.txt -files that are produced after each run, it is possible to evaluate the costs induced by the usage of inclusion/exclusion masks (see also section 2.6 Replacement cost analysis).

3.6 Post-processing analyses & options

This chapter includes descriptions for the three different types of analyses, that can be conducted for solutions produced from the main Zonation runs. These three groups are:

1. Post-processing analyses, which can be done manually from the Zonation windows interface. These include
   - Landscape identification
   - Statistics for management landscapes
   - Solution comparison
   - Fragmentation uncertainty analysis
2. ZIG Summary utility, which is run by a separate ZIG_Sum program (comes together with the Zonation program).
3. Solution cross-comparison using loaded solutions.

3.6.1 Landscape identification

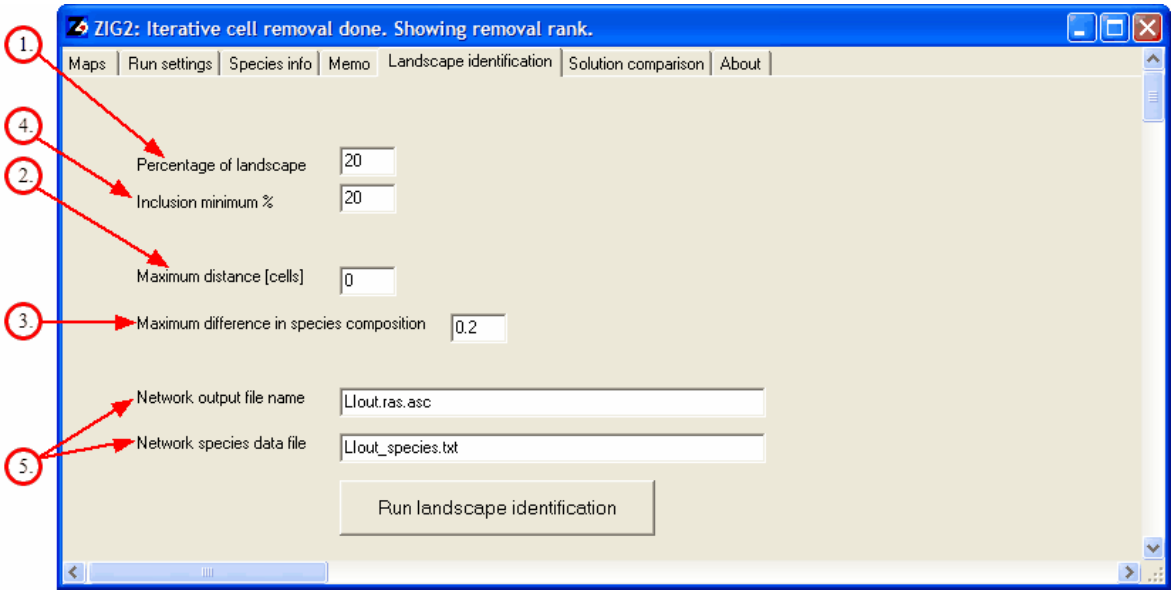
This process is also explained in Moilanen *et al*. 2005 (*Proc. R. Soc. B* **272**, p. 1886→ and figures 2 and 3).

This option allows identification of separate management landscapes based on the distance and similarity in species composition between two sites. Spatially distinct areas (consisting of multiple grid cells) in a Zonation solution can be classified into management landscapes. An area is joined to a landscape if it is close enough and similar enough in the species composition to *any* other distinct area in the same landscape. Landscape identification is done for a given fraction of the landscape.

© 2004-2006 Atte Moilanen

Running landscape identification

The landscape identification can only be done from the windows interface. Being a post-processing analysis, you first need to run the Zonation analysis with your data or load an old solution (.rank.asc -file) in the Run settings -window.



1. First define the **percentage of landscape**. This will determine how large part of the entire landscape will be included in the classification. Note that the percentage here means the top fraction of the landscape. E.g. value of 20% includes the best 20% area from the landscape to the solution.

2. Give the nearest neighbour **maximum distance** (in cells!), which is allowed between patches that are included in the same management landscape. E.g. a maximum distance of 0 would mean that all separate groups of cells are identified as unique management landscapes.

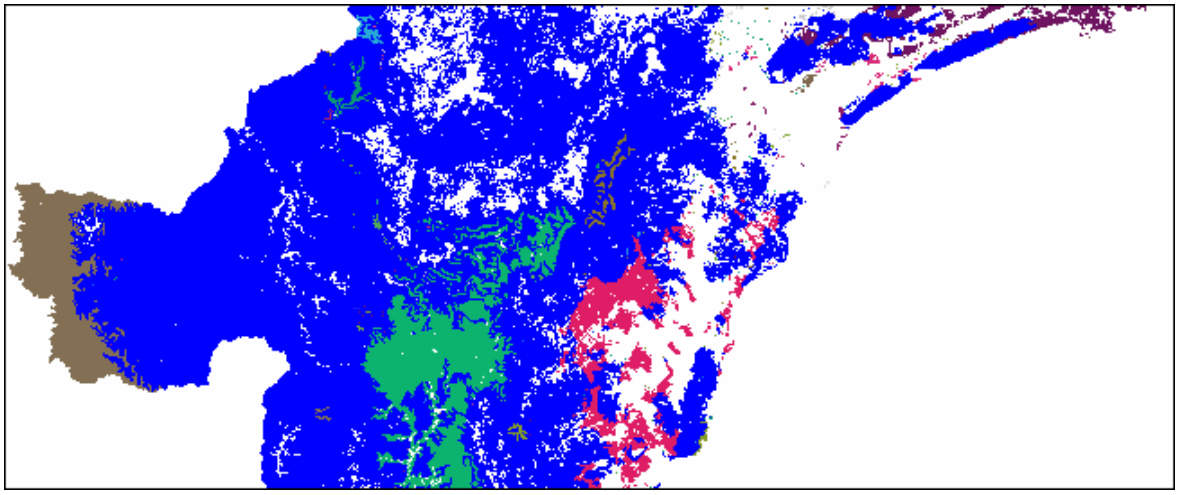
3. Give the **maximum difference in species composition.** This determines how much the species compositions between two cells are allowed to differ (in terms of relative densities) for them to be joined to the same landscape. A value of 0 indicates that the species composition in two patches is identical. Value of 1 indicates that the difference in relative density between two patches is on average log10 across species. E.g., a maximum difference of 0.2 means that on average two species out of ten have a 1-log difference in their density or that one tenth of all the species have a 2-log difference. For more details, see Moilanen *et al*. (2005).

4. Define **inclusion minimum**, which in turn determines how highly ranked cells must be included in each management landscape. E.g. value of 10% means that each management landscape has to contain at least one cell which belongs to the top 10% fraction of the whole landscape. Thus, this option can be used for setting criteria for the management landscapes. Note that if the inclusion minimum is equal to (or larger than) the **percentage of landscape**, all spatially separate areas will be included in the management landscapes, where as if the inclusion minimum is smaller, then only areas with sufficiently high ranked cells are included.

5. Finally, define the names of your output files to **Network output file name** and **Network species data file** fields.

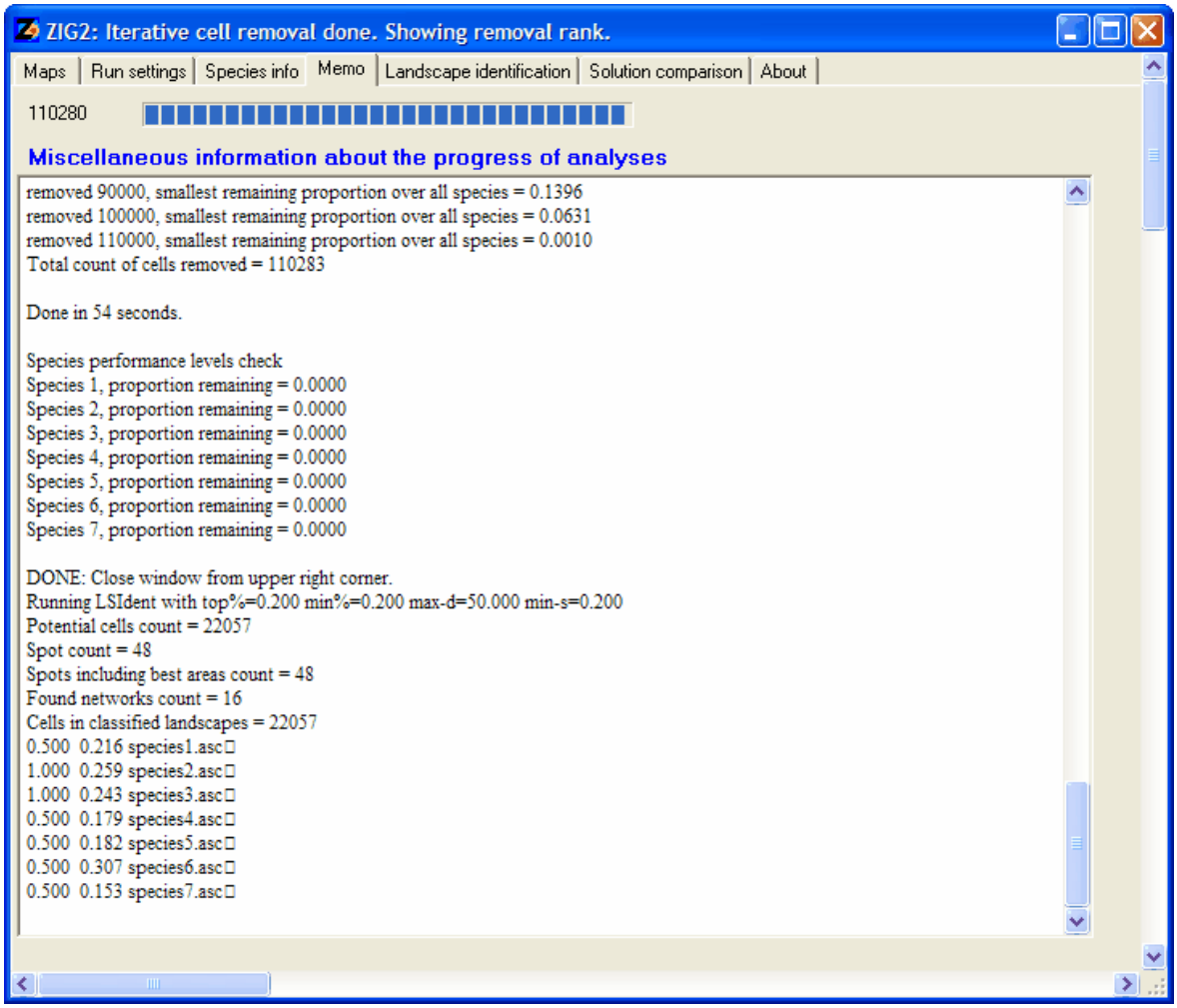
© 2004-2006 Atte Moilanen

Output



A picture of landscape identification output map.

Running the landscape identification produces a map, which shows you the separate landscapes in different colors. Areas that were not included in the selected top fraction (see "Percentage of landscape" above) are shown in blue. The colors in landscape identification output have no special interpretation - they are random colors for distinguishing the separate landscapes from each other.


ZIG2: Iterative cell removal done. Showing removal rank.
Maps
Run settings
Species info
Memo
Landscape identification
Solution comparison
About
110280
Miscellaneous information about the progress of analyses
removed 90000, smallest remaining proportion over all species = 0.1396
removed 100000, smallest remaining proportion over all species = 0.0631
removed 110000, smallest remaining proportion over all species = 0.0010
Total count of cells removed = 110283
Done in 54 seconds.
Species performance levels check
Species 1, proportion remaining = 0.0000
Species 2, proportion remaining = 0.0000
Species 3, proportion remaining = 0.0000
Species 4, proportion remaining = 0.0000
Species 5, proportion remaining = 0.0000
Species 6, proportion remaining = 0.0000
Species 7, proportion remaining = 0.0000
DONE: Close window from upper right corner.
Running LSIdent with top%=0.200 min%=0.200 max-d=50.000 min-s=0.200
Potential cells count = 22057
Spot count = 48
Spots including best areas count = 48
Found networks count = 16
Cells in classified landscapes = 22057
0.500 0.216 species1.asc
1.000 0.259 species2.asc
1.000 0.243 species3.asc
0.500 0.179 species4.asc
0.500 0.182 species5.asc
0.500 0.307 species6.asc
0.500 0.153 species7.asc

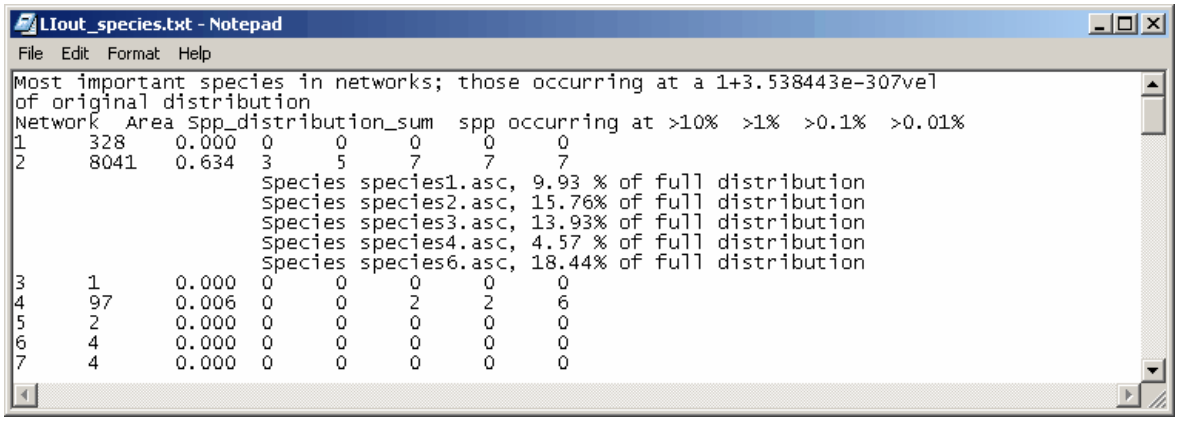
© 2004-2006 Atte Moilanen

In addition the landscape identification produces a basic raster output file:

.ras.asc file Here the matrix indicates which cells belong to which management landscapes. Each landscape has an integer starting from number one. If a cell has a value of -2, it means that the respective cells has not been included in the given top fraction (see "Percentage of landscape" above). Remember that this file, as any of the ASCII files produced with Zonation, can be imported to GIS programs. However, when importing this file, **select integers** as the format of you cell values!

3.6.2 Statistics for management landscapes

The landscape identification procedure also produces a text output file (network species data) containing statistical information of the management landscapes.


LIout_species.txt - Notepad
File Edit Format Help
Most important species in networks; those occurring at a 1+3.538443e-307vel
of original distribution
Network Area Spp_distribution_sum spp occurring at >10% >1% >0.1% >0.01%
1 328 0.000 0 0 0 0 0
2 8041 0.634 3 5 7 7 7
Species species1.asc, 9.93 % of full distribution
Species species2.asc, 15.76% of full distribution
Species species3.asc, 13.93% of full distribution
Species species4.asc, 4.57 % of full distribution
Species species6.asc, 18.44% of full distribution
3 1 0.000 0 0 0 0 0
4 97 0.006 0 0 2 2 6
5 2 0.000 0 0 0 0 0
6 4 0.000 0 0 0 0 0
7 4 0.000 0 0 0 0 0

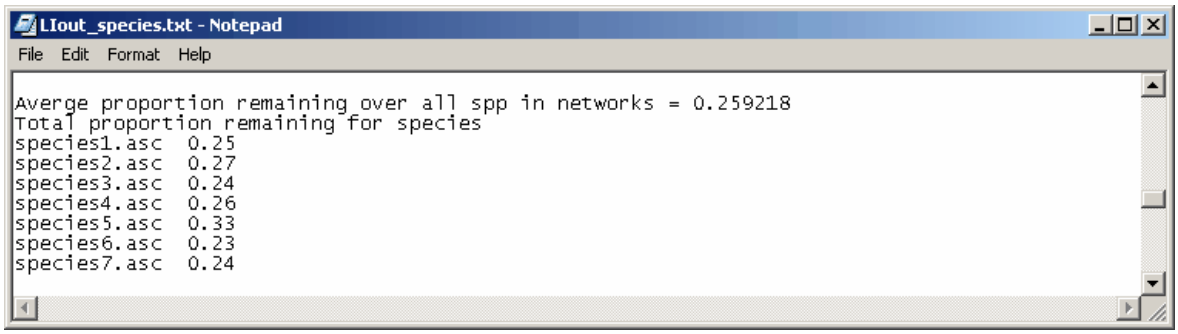
With the file you can receive a set of information about the different management landscapes in your data. **The first part** of the file contains statistics about species occurrences in each landscape. This part is divided to eight columns:

1. Number of the management landscape.
2. Area of the management landscape in cells.
3. Sum of species distribution proportions. In other words this value shows how large proportions of species **original** distributions the respective management landscape covers.
4. Number of species which have more than 10% of their original distribution located in the management landscape.
5. Number of species which have more than 1% of their original distribution located in the management landscape.
6. Number of species which have more than 0.1% of their original distribution located in the management landscape.
7. Number of species which have more than 0.01% of their original distribution located in the management landscape.
8. Number of species which have more than 0.001% of their original distribution located in the management landscape.

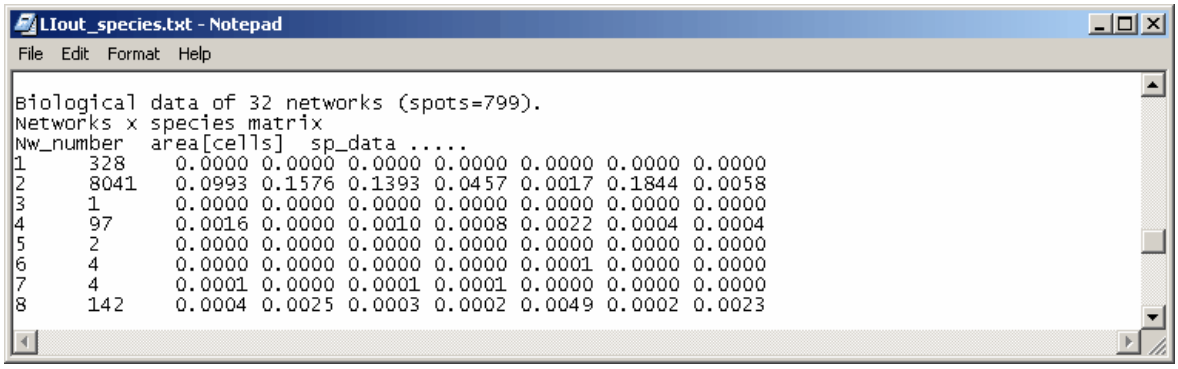
If the five last columns are marked as zero, it means that in that particular management landscape the species occurrence is less than 0.01% of their full distribution. Note that if any of the species have a larger proportion than 1% of its distribution located in the landscape, the program automatically prints a list of those species and the precise proportions of their distributions on the next rows.

The second part shows you how large proportions of species distributions are remaining in the whole landscape (all management landscapes together), that was initially included in to the analysis (see section 3.6.1, Percentage of landscape). The program also automatically calculates an average of these proportions.

© 2004-2006 Atte Moilanen



The third part contains a list of all management landscapes, area in number of cells and the proportions of distributions for each species in the respective management landscape. The species are listed here in the same order as they are in your species list file.



Note that setting the maximum distance between cells to zero allows you to view the statistics of every single spatially distinct patch in the landscape, but also increases the running time. A larger maximum distance leads to fewer management landscapes. Note that the program presently only allows identification of up to 30 000 landscapes.

3.6.3 Solution comparison

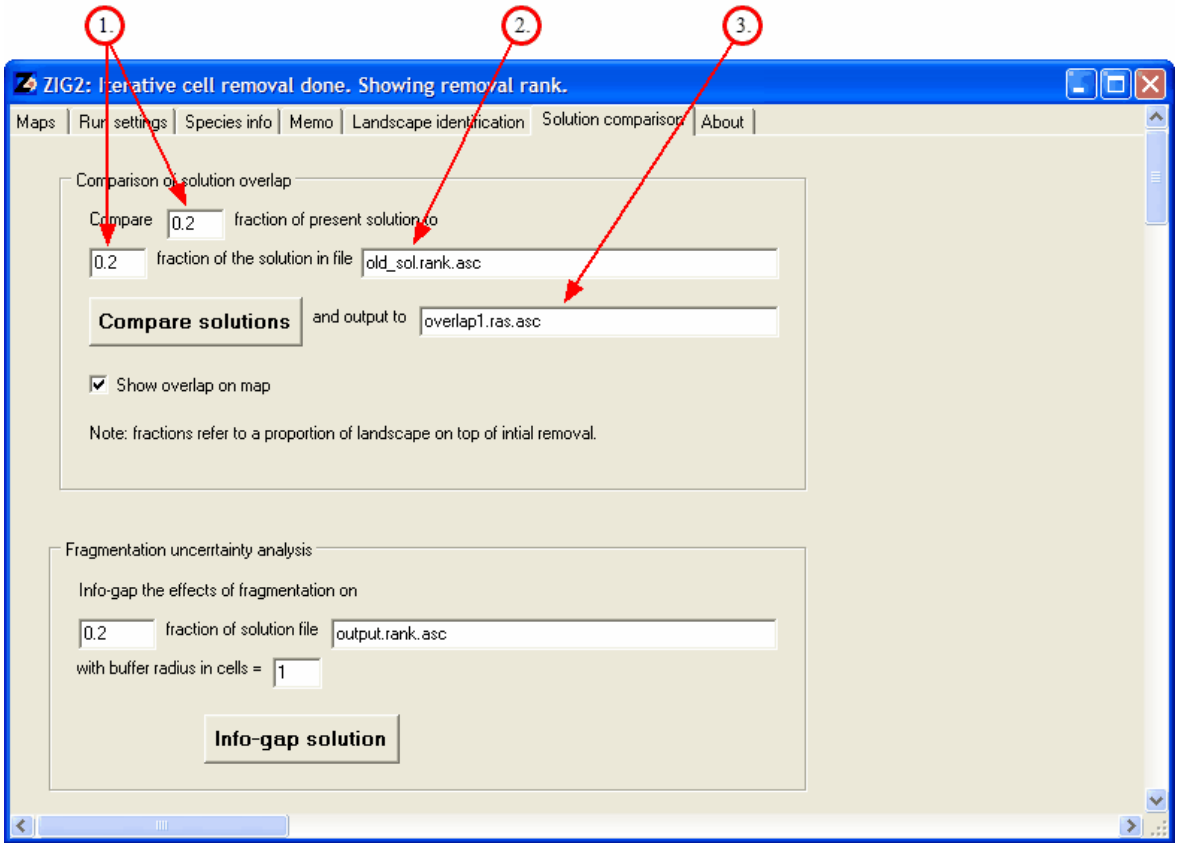
Solution comparison calculates how much two solutions overlap with each other and what is the average difference in the cell removal order. The comparison is always made between the present solution and an older solution by using the rank.asc -files of both solutions as input files.

Running solution comparison

The solution comparison can only be done from the windows interface.

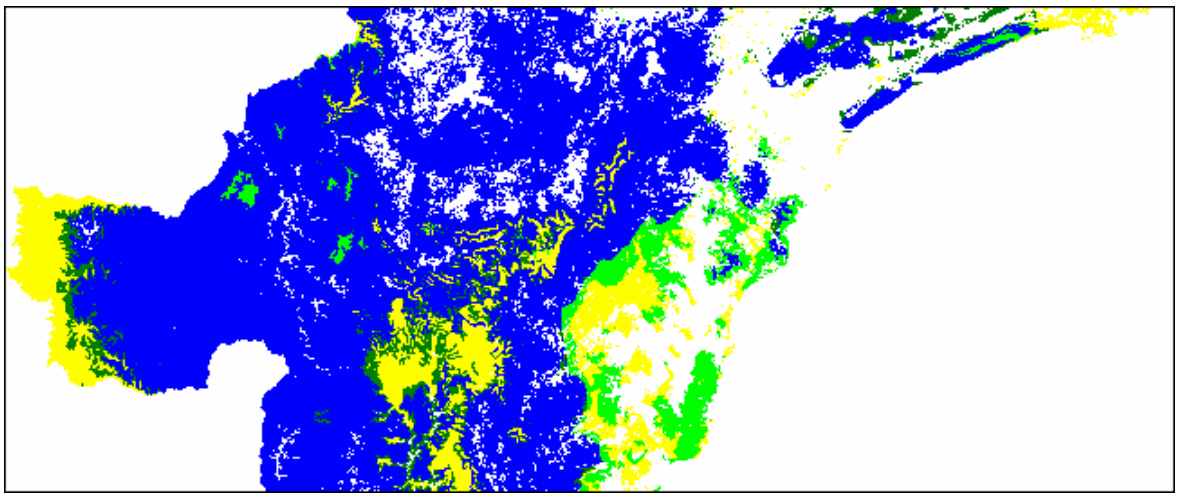
1. First, go to the **Solution comparison -window** and select how large proportion of each landscape is compared ("Compare ... fraction of present solution to ... fraction"). Note that if a part of the landscape was initially removed when running the basic Zonation (see section 3.3.2.3, Run settings), the selected percentage will be out of the part remaining after initial removal. I.e. if initial removal is 0.5 and 0.2 is selected for landscape comparison, the area used in the comparison will be only 10% of the entire landscape.
2. Next, define the name of the rank-file to which the current solution is compared.
3. Finally, give a name to your output file, e.g. "overlap1.ras.asc", and press the "Compare solutions" -button.

© 2004-2006 Atte Moilanen



Output

The program produces a map showing the results of the comparison. Here all overlapping areas are shown in yellow, where as the light green areas are only included in the present solution and the dark green areas are only included in the older solution. The rest of the landscape (not included in the selected top fraction) is coloured as blue. **Note that this map is not automatically saved.** If you wish to save it, double click on the image.



Picture of the output map.

More detailed results can be found in the Memo -window. Here, the settings of your analysis and the similarity of the two solutions (f1 and f2) is shown. "Average order diff" is the average difference in removal rank order between the two solutions.

The Solution comparison also produces a basic raster output file (ras.asc -file).

© 2004-2006 Atte Moilanen

.ras.asc -file The values in the matrix are as follows:

0. The cell is not included in the top fraction
1. The cell is included in both solutions (overlapping areas marked as yellow)
2. The cell is included only in the present solution (light green areas)
3. The cell is included only in the older solution (dark green areas)

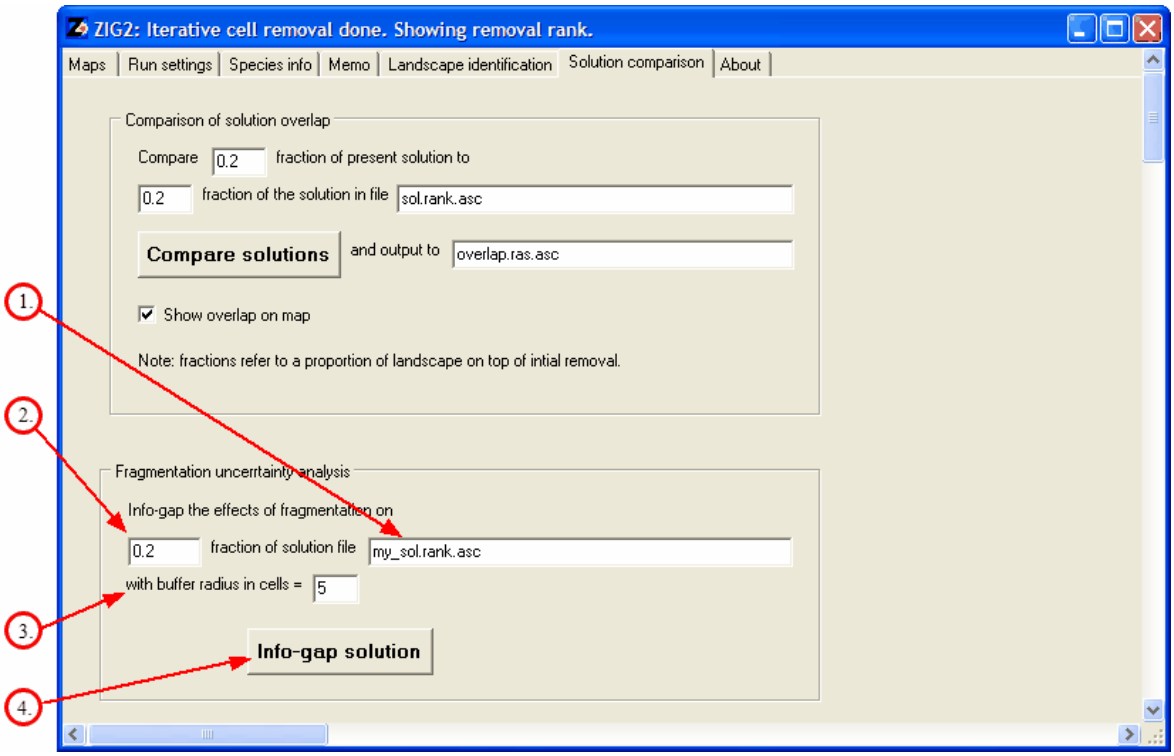
Remember that this file, as any of the ASCII files produced with Zonation, can be imported to GIS programs. However, when importing this file, select integers as the format of your cell values!

3.6.4 Fragmentation uncertainty anlysis

The theory behind fragmentation uncertainty analysis is explained in section 2.5.2. This analysis is also described in Moilanen & Wintle (2005) *Biol. Conserv.* **129**: 428-430.

It has been widely argued that habitat fragmentation is bad for population persistence and that a high level of fragmentation is a similarly undesirable characteristic for a reserve network. In this analysis it is assumed that cells deep inside a reserve will not be influenced by habitat loss around the edges of the reserve. Cells close to the edge, on the other hand, may lose some of their biological value due to known and unknown negative effects of nearby habitat loss and fragmentation. The higher the proportion of habitat lost around the cell, the less certain one would be of the remaining conservation value. **Fragmentation uncertainty analysis** provides a method to see how different conservation network structures respond to surrounding habitat deterioration and thus helps you to evaluate the robustness of your reserve network candidates against negative effects of habitat fragmentation.

Running Fragmentation uncertainty analysis



The Fragmentation uncertainty analysis can only be done from the windows interface.

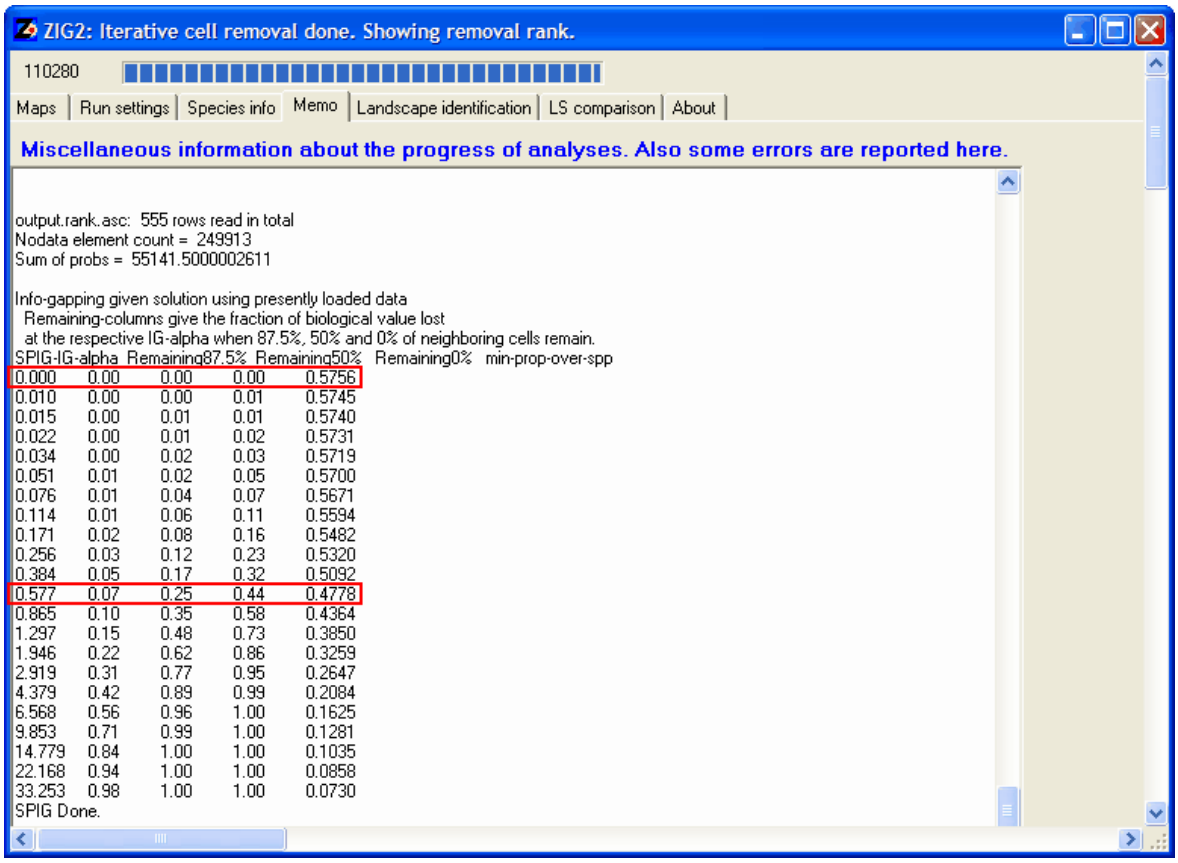
1. Go to **Solution comparison -window** and type the name of your solution rank file (.rank.asc -file, one of the output files in basic Zonation analysis).
2. Determine how large fraction of the landscape will be included in the analysis.
3. Next, set the buffer radius. This determines the area around a cell in which any loss of habitat will influence the biological value of the focal cell. Size of the buffer radius depends on your conception of how far negative effects of fragmentation might reach, but also on

© 2004-2006 Atte Moilanen

the cell size of your data, as the length of radius is given in number of cell.

4. Finally, press the "Info-gap solution" -button to initiate the computation.

Output


ZIG2: Iterative cell removal done. Showing removal rank.
110280
Maps
Run settings
Species info
Memo
Landscape identification
LS comparison
About
Miscellaneous information about the progress of analyses. Also some errors are reported here.
output.rank.asc: 555 rows read in total
Nodata element count = 249913
Sum of probs = 55141.5000002611
Info-gapping given solution using presently loaded data
Remaining-columns give the fraction of biological value lost
at the respective IG-alpha when 87.5%, 50% and 0% of neighboring cells remain.
SPIG-IG-alpha Remaining87.5% Remaining50% Remaining0% min-prop-over-spp
0.000 0.00 0.00 0.00 0.5756
0.010 0.00 0.00 0.01 0.5745
0.015 0.00 0.01 0.01 0.5740
0.022 0.00 0.01 0.02 0.5731
0.034 0.00 0.02 0.03 0.5719
0.051 0.01 0.02 0.05 0.5700
0.076 0.01 0.04 0.07 0.5671
0.114 0.01 0.06 0.11 0.5594
0.171 0.02 0.08 0.16 0.5482
0.256 0.03 0.12 0.23 0.5320
0.384 0.05 0.17 0.32 0.5092
0.577 0.07 0.25 0.44 0.4778
0.865 0.10 0.35 0.58 0.4364
1.297 0.15 0.48 0.73 0.3850
1.946 0.22 0.62 0.86 0.3259
2.919 0.31 0.77 0.95 0.2647
4.379 0.42 0.89 0.99 0.2084
6.568 0.56 0.96 1.00 0.1625
9.853 0.71 0.99 1.00 0.1281
14.779 0.84 1.00 1.00 0.1035
22.168 0.94 1.00 1.00 0.0858
33.253 0.98 1.00 1.00 0.0730
SPIG Done.

The results of the analysis will appear in the Memo -window. The **first column** shows the value of α, which is the info-gap uncertainty parameter. The α –value represents the uncertainty of species occurrence in cell, in other words the uncertainty that the species does not occur in a specific cell although our data suggests that it does. The higher the α –value, the higher the uncertainty. In the picture above an α –value of 0.000 on the first row indicates, that the observed occurrence of a species in a given cell is trusted to be completely accurate. The increasing α results in rapid **potential** loss of biological value in target cells as neighbourhood habitats are lost.

The **following three columns** indicate (for any given α) the loss of biological value in the focal cell when 87.5%, 50% or 0% of the neighbourhood habitat is remaining, respectively. The **fifth column** shows how large proportions of species distributions are actually remaining in your reserve network when you take the uncertainty effect into consideration (V_s), but when there is yet no fragmentation. **Note that here again the value indicates the proportion of distribution for the worst-off species**. Thus, other species may have a larger proportions remaining.

For example, from the picture above we can see that when α has a value of 0.000 (= no uncertainty) each species has at least 57.56% of their distribution remaining in the landscape. But as the α –value increases up to e.g. 0.577, the minimum proportion of species distribution in the very same landscape decreases to 47.78%. In addition, the level of fragmentation amplifies the loss of biological value in single cells. When 87.5% of the neighbourhood habitats are remaining, the biological value of a focal cell has decreased by 7%. When 50% of habitats are remaining, the biological value has decreased by 25% etc.

But how to determine the value of uncertainty? The answer to this is that *α* has no correct value - the range of α –values that are of interest depends on how much certainty is required. The main

© 2004-2006 Atte Moilanen

question here is what happens when you increase the value of α? As mentioned earlier, the primarily goal of this method is to compare the performance of different network candidates in the light of increasing uncertainty. If a network has a spatial structure that is resistant to negative effects of neighboring habitat loss, then the performance of the network is relatively insensitive to an increasing α . If the proposed network has a spatial pattern that is sensitive to potential negative effects of habitat loss, then the performance of the network degrades rapidly as α increases. This would be the case when locally high quality locations are right at the edge of the proposed network, which suggests that habitat loss outside the reserve could well influence what happens just inside the reserve at the locally valuable places.

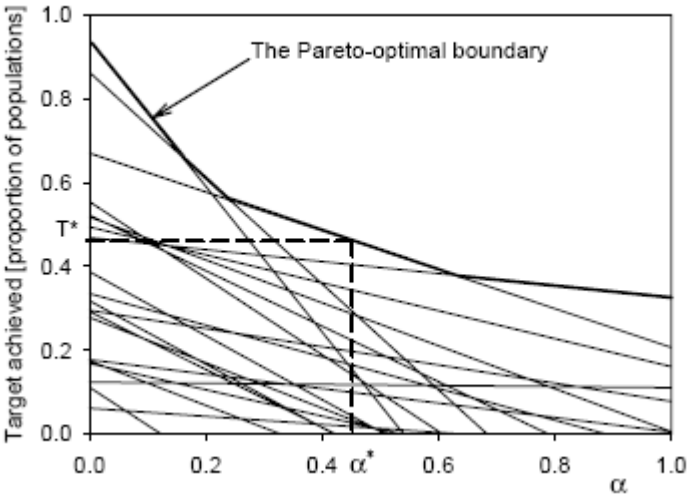


Figure showing the performance of different networks when α is increased. The Pareto-optimal line indicates best candidates at all levels of α .

3.6.5 ZIG_Sum Utility

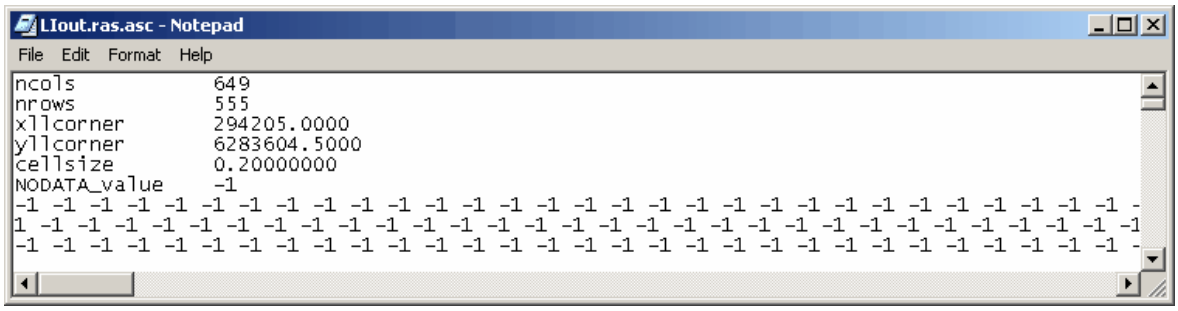
This analysis is also described in Moilanen *et al.* (2006) *Conserv. Biol. 20: 1688-1697.*

Essentially, the ZIG_Sum utility does an analysis of selection frequency. As concluded so far, you might get varying solutions for your data by using different settings (e.g. weights, α –values) or additional utilities (BQP, UCA). With ZIG Summary you can compare these several solutions and find out which areas in the landscape are most often included in the final solutions and thus have the highest conservation value regardless of the analysis settings.

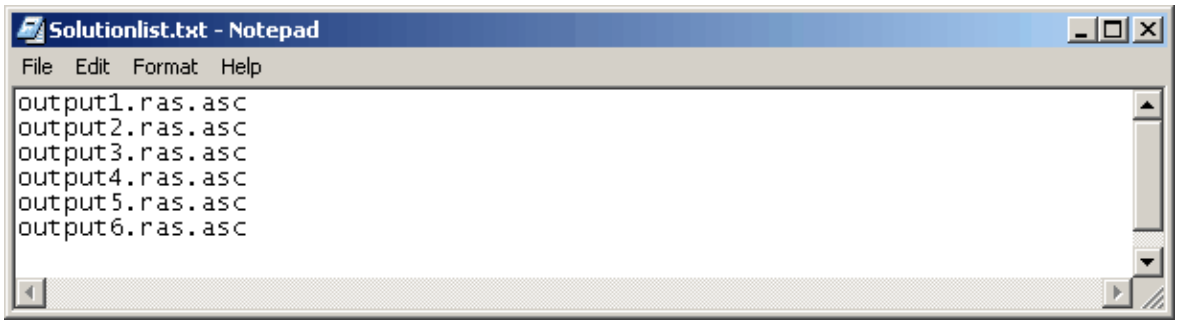
Input files

ZIG Summary uses raster files that have been produced with the Landscape identification utility in the Zonation. Note that **all raster files should include the same proportion of the original landscape**, otherwise the analysis may become difficult to interpret. Thus, when producing the landscape identification rasters, the value in the "Percentage of landscape" -field should be equal in all runs. **Also the "Inclusion minimum percentage" needs to equal with the "Percentage of landscape" -value**. This is to ensure that all areas in the given fraction are identified in the solution.

© 2004-2006 Atte Moilanen



In addition to the rasters you need a .txt -file which contains a list of all the landscape identification files. All input files should either be in the same directory with the ZIG Summary program or you should type the path to the correct directory in front of the file names.



Note that technically there is no reason why the proportions of original landscape should be equal in all raster files. The program will run regardless of the settings, but the interpretation of results changes if different fractions are used.

Running ZIG Summary

ZIG Summary can only be run from the command prompt:

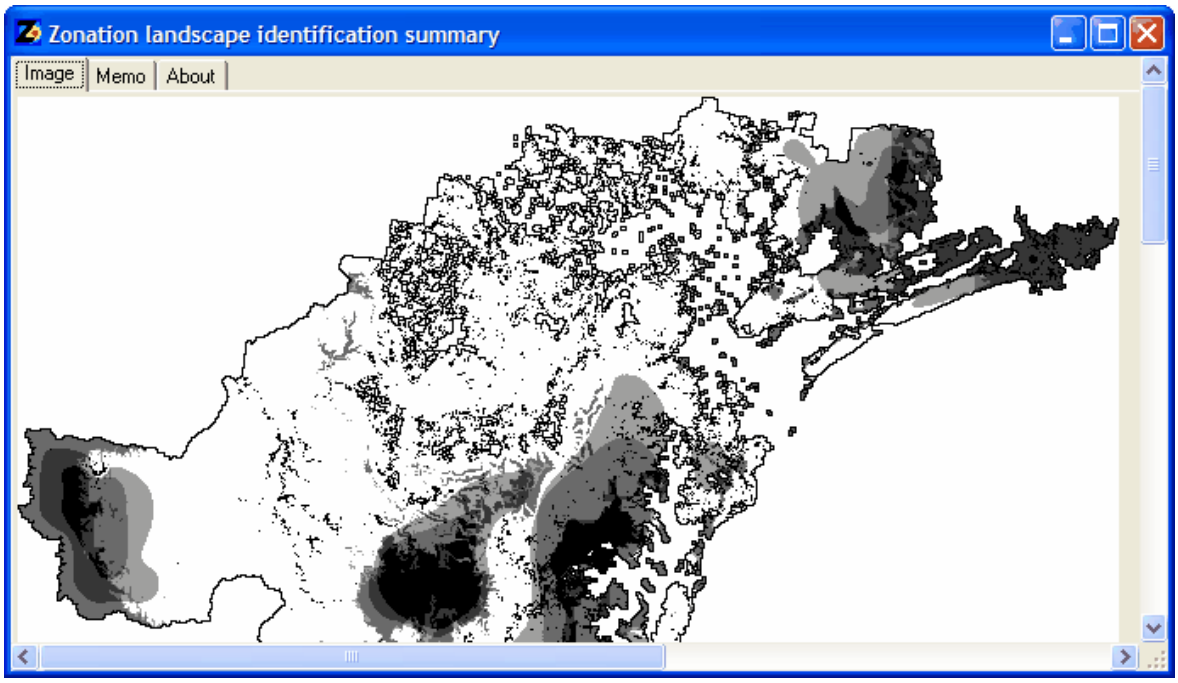
1. Open a new .txt file (for example with notepad) and type the following command in it:
   ```
   zig_sum solutionlist.txt output.asc 0 map.jpg
   ```
   First parameter is the name of the program. **Second parameter** is the name of the .txt -file where you have a list of your landscape identification solutions. For **third parameter** enter a suitable name for your output raster data (.asc -file). **Fourth parameter** determines the layout of your output map, value 0 resulting a grey scale picture and value 1 resulting in colour picture. For **fifth parameter** enter a proper name for your output map (.jpg -file).
2. Save the file as .bat file (e.g. dozigsum.bat) in the same directory, where you have the ZIG Summary program. Note again that the file name extension of a batch file has to be **.bat**. If there is anything else after the .bat -suffix, Windows cannot identify the file as a command file.
3. Open command prompt and go to the directory, where you have the ZIG Summary program. Type the name of your .bat file (without the suffix) and press enter.
4. Another way to run the program is to simply double click the batch file from windows.
5. You can edit the batch file using notepad or the command prompt edit command.

Output

As the program starts to run, a separate ZIG Summary window appears on the screen. In the **Image** -window the program first quickly displays all those solutions, which are included in the analysis and then runs the comparisons. After the program has finished, it displays a map where most valuable areas are shown in grey scale. In other words these are the areas, which in most

© 2004-2006 Atte Moilanen

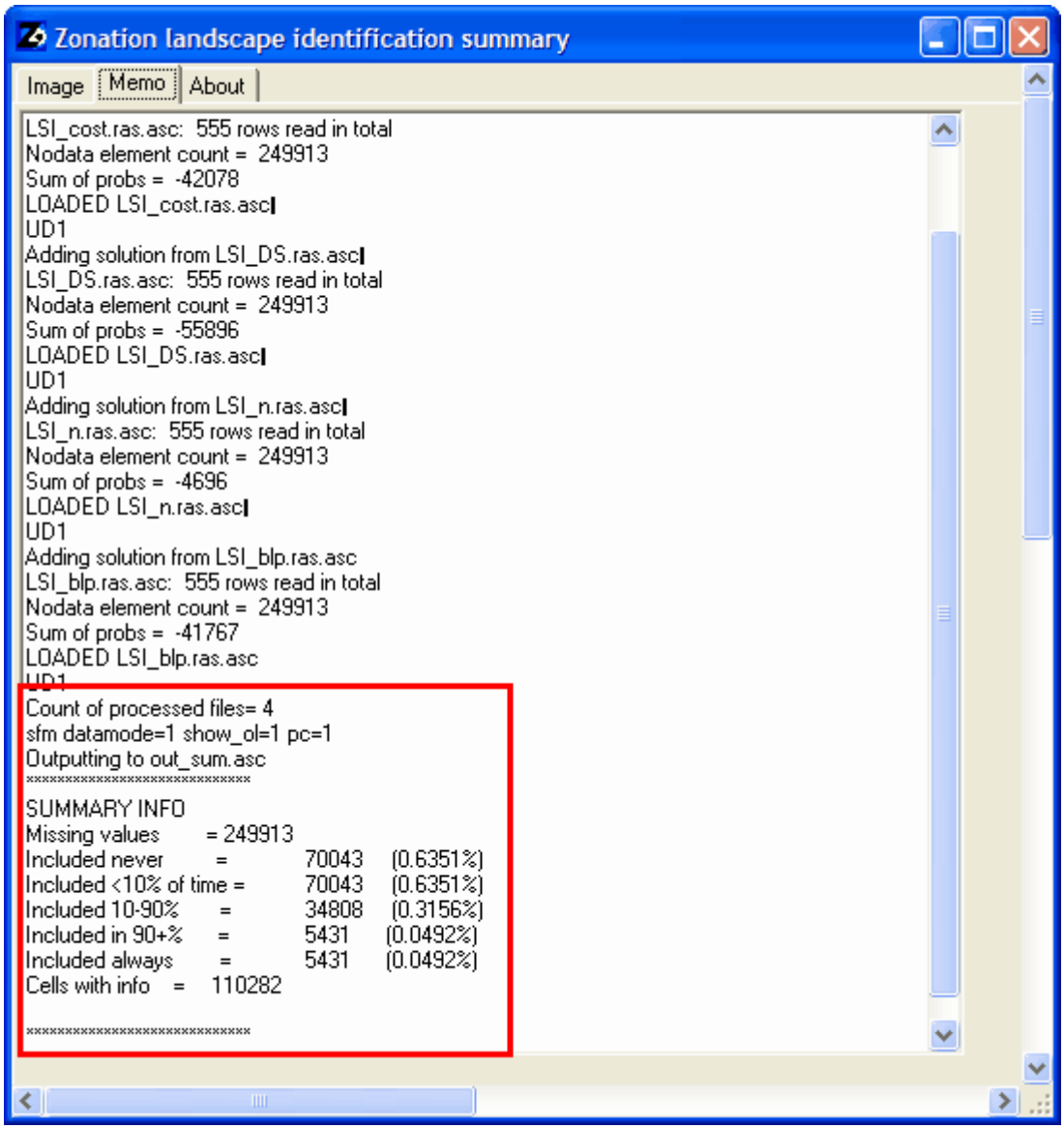
cases are included in your solutions. Note that when using the grey scale settings, most valuable areas are shown as black, where as with coloured settings, most valuable areas are shown in white. This map will automatically be saved as your **output .jpg file**, but you can save it again (e.g. with a different name or to a different directory) by double clicking the picture.



The Image -window showing an example of the ZIG Summary output map, when the layout settings have been adjusted to grey scale.

The Memo keeps track of what the program has been doing. At the end of the memo you can find a summary of your results, e.g. how many cells where included in to the solutions in more than 90% of the cases, how many cells were never included, etc. In the parentheses are the proportions of each cell group. Note, that the group <10% also contains those cells, which were never included in the solutions where as the group 90+% contains the cells, which were always included.

© 2004-2006 Atte Moilanen



Running ZIG Summary also automatically produces a standard format **output raster file** (.asc -file), which represents the hierarchy of the cells. Here the value of each cell indicates how many times that particular cell has been included in the solutions (as a proportion of all solutions). Remember again that this file can be imported to GIS programs. When importing, select floating values (not integers) as the type of your data.

3.6.6 Solution cross-comparison using solution loading

This analysis is used, for example, in figure 4 of Moilanen & Wintle (2007), where effects of BQP on solutions originally calculated with the BLP are evaluated.

When loading an old solution the program does not just display the solution, but removes cells from the landscape based on the ranking order of the old solution. Thus it is possible to test the performance of one network with different settings, using new settings to evaluate the solution. You can, for example, run the basic Zonation and then test how well the resulted network would perform, if uncertainty or boundary quality penalty would be included in the analysis.

To do this you need to load your old solution with new settings (see section 3.2.4 for instructions). If you are running the program from the windows interface, you can adjust the settings in the **Run settings -window**. Then, select the "Load old solution .rank file" -option and type the name of

© 2004-2006 Atte Moilanen

your ranking file on the field below. If you are operating the program from command prompt, type "-lfilename" as the second parameter of your call. Remember also to enter the correct name of your adjusted settings file as the third parameter in your call.

You can see the results, for example, in the **species info** curves in the windows interface. You can also compare the curves.txt files of the two solutions which reveal how large proportion of distribution of each species is remaining when landscape is iteratively removed.

3.7 Tips for using the command prompt

Here is a list of some basic commands that are useful when operating the command prompt:

`help`	Prints a list of most common commands and their explanations. You can also view descriptions for specific commands by typing "`help command_name`".
`cd`	Shows the name of your current directory. You can move to another directory by typing "`cd directory_name`".
`cd..`	Moves one level up in the directory tree.
`md`	Creates a new subdirectory. Type the name of your new directory after the command, i.e. "`md new_directory`"
`dir`	Prints a list of all files in your current directory. You can narrow the list to certain type of documents by typing an asterisk and the suffix after the command. E.g. if you are searching for a text file, type "`dir *.txt`" and only .txt files will be shown. Or "`dir a*.txt`" .txt file that start with an 'a'.
`dir /od`	Prints a list of all files and documents in chronological order.
`dir /ad`	Prints a list of all subdirectories in your current directory.
`edit`	Command to edit documents. Write the name and suffix of your document after the command, e.g. "`edit my_document.txt`". This is a useful command for editing your list or settings files.
`notepad`	Opens a respective document with Notepad -program. Write the name and suffix of your document after the command, e.g. "`notepad my_doc.txt`".
`copy`	Copies one or several files to another directory. For example, command "`copy file1.txt my_docs\file1.txt`" copies the file "file1" to directory "my_docs". Command "`copy file1.* my_docs\*.*`" copies all files with the name "file1" into the directory "my_docs" with their original names and formats. You can also copy your files under a new name, i.e. with command "`copy file1.* my_docs\file2.*`" all files are copied to the directory with a new name "file2".
`rename`	Renames a file. After the command type the name of the file you whish to rename and then the new name for that file. I.e. "`rename old_name.txt new_name.txt`"
`type`	Prints the contents of a text file in the command prompt.
`doskey`	Edits command lines, calls Windows commands and creates macros. A useful tool which allows you, for example, to move back and forward in your commands with the cursor moving keys. Thus you do not need to repeat same commands by writing them time after time, pressing the arrow up key displays all recently used commands. To activate the tool write "`doskey`" and press enter.
`call`	Calls a program inside a batch file. E.g. "`call zig2`".
`rem`	With this command you can enter comments into your batch files.
`exit`	Closes the command prompt.

3.8 Troubleshooting

Here is a short list of things to check, when encountering problems:

- α –**values**
  Check the α –values for any errors. Remember that these values have to be in **same unit of length** as the cell size given in the species distribution map file.

© 2004-2006 Atte Moilanen

- **Empty rows at the end of your input files**
  Check that you do not have any empty rows at the end of your input files. These may cause some unexpected software behaviour.

- **Decimal points and commas**
  Always remember to use only decimal points! NO commas!

- **Differences in grid sizes/cell sizes**
  All raster files should have the same grid size. This means that in all files the number of columns and rows as well as the size of cells should be equal. You can check these information from the beginning of each raster file.

- **No data -rows at the edges of species distribution matrixes**
  Computational efficiency requires the input data to have at least one row of no data on each edge of your species distribution grids. Otherwise the program will automatically transform all values on the edge rows to missing data.

- **Differences in grid matrixes between species distribution files**
  This might be a problem when you are using boundary quality penalty. Remember to select the correct BQP mode based on the alignment of your species distribution data. If you are getting odd values when running the BQP (e.g. values for species distribution remaining in the landscape are negative or increasing as cells are removed), you most likely have non-uniform species data and you have chosen the wrong BQP mode (i.e. mode 1). The correct BQP mode for non-uniform data is mode 2, which is slower and uses more memory.

- **Differences in grid matrixes between species distribution and other data files**
  Check that all species distribution rasters are congruent with any other raster files used in analysis (e.g. cost layer, uncertainty layers etc.) This means that all those cells in a grid which have data for any of the species used in the analysis (that is to say, the cells that are NOT marked as "no data" in all species distribution files), also have to have a value in the optional raster grids. Equally, all cells marked as "no data" in all species distribution rasters should have the same definition in any optional rasters.

- **Directory paths**
  Check that you have entered the correct paths to your files, so that the program can find them. If you have the program in the same directory with your input files, you do not need to type the paths, just the file names. However, if some/all of your input files are located some where else, a directory path is needed for these files.

- **File names**
  One reason for problems can be the long directory and file names, especially if you are using the command prompt. Thus try to keep the directory names short (e.g. max. 8 marks). Also, do not use any spacings in your directory or file names.

- **Computer memory capacity**
  If the program is running slow during computations, check Task Manager/Performance. If your RAM (Physical Memory) has decreased towards zero, you are running out of memory. This does not mean that the program has jammed, but it will take a couple of lifetimes for it to finish up the calculations. In other words, stop the computation and try again after closing all other programs to save memory, or with a smaller data set or with a computer that has more memory. See section 3.9 for more detailed information related to computer memory capacity.

- **Check the memo**
  Some warnings or error messages appear in the memo. Read through the text to check for any information that might give a clue to solving your problem.

© 2004-2006 Atte Moilanen

3.9 Assumptions, limitations & system requirements

Hardcoded limitations

All analyses
- Maximum number of species 2 000

Distribution smoothing
- Maximum size of rasters 16 mil. elements (4 000 x 4 000)

Boundary Quality Penalty (BQP)
- Maximum number of penalty curve profiles 50
- Maximum number of points on a penalty curve 20
- Maximum number of different species-specific buffer sizes 100

Landscape identification
- Maximum number of management landscapes 30 000

Memory requirements

Memory requirements depend on the data you are using. Naturally, the larger the data (many species and/or high resolution and/or large landscape), the more memory you will need to run the computations. One raster file of 1 million elements (cells that have real data, not missing values) for one species requires 4 MB of memory. Thus you can roughly calculate the maximum number of species that you can use with the help of this formula:

Max. species = 0.7 * memory in MB / (4 * grid size [in millions of elements])

The 0.7 in the formula accounts for the memory needs of the operating system and the memory needs of Zonation in addition to the species data matrixes. Thus with 4 GB (= 4 000 MB) of memory you can have approximately (0.7 * 4 000)/(4 * 5) = 140 species with 5 mil. informative grid elements. Using BQP mode 2 (species-specific missing data areas) approximately triples the memory consumption compared to an analysis with no BQP used, leading to a respective loss in the number of species that can be sued in the analysis.

3.10 Known software problems and bugs

This is the first version of this documentation and software. Thus, we are not aware of bugs at this time. Good luck with it!

© 2004-2006 Atte Moilanen

Part

4 Tutorial & Examples

The installation package includes the following example files:

For running basic Zonation
- species1.asc
- species2.asc
- species3.asc
- species4.asc
- species5.asc
- species6.asc
- species7.asc
- splist.spp
- splist_abf.spp
- splist_tbp.spp
- cost.asc
- set.dat
- set_cost.dat
- do_zig2.bat
- do_load.bat

For weighting species
- splist_w.spp
- do_w.bat

For including distribution smoothing
- do_ds.bat

For including BQP
- BQPcurves.txt
- splist_bqp.spp
- set_bqp.dat
- do_bqp.bat

For including BLP
- set_blp.dat
- do_blp.bat

For including uncertainty analysis
- sp1_UC.asc
- sp2_UC.asc
- sp3_UC.asc
- sp4_UC.asc
- sp5_UC.asc
- sp6_UC.asc
- sp7_UC.asc
- UCweights.spp
- set_uc.dat
- do_uc.bat

For running the replacement cost analysis
- mask_rs.asc
- mask_towns.asc
- set_maski.dat
- set_maske.dat
- do_rs.bat
- do_towns.bat

© 2004-2006 Atte Moilanen

Other files needed for tutorial and exercises
- set_costds.dat
- set_costbqp.dat
- load_costds.bat
- load_costbqp.bat
- do_cost_ds.bat

© 2004-2006 Atte Moilanen

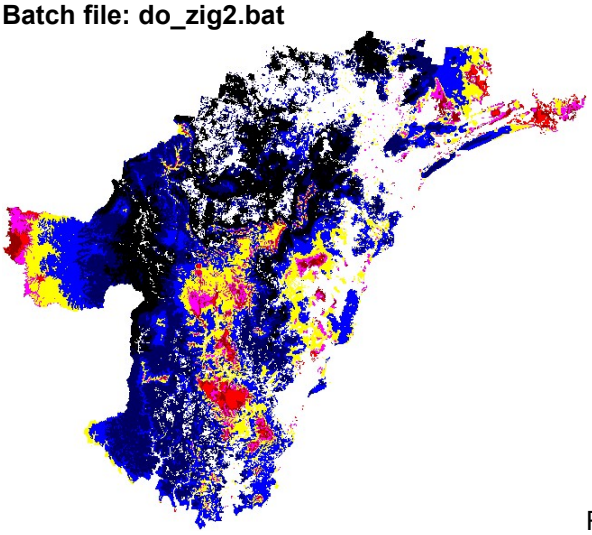
Exercise 1. Getting started with the basic Zonation

Before starting see section 3.2. for how to operate the program either from command prompt or windows interface.

We start with a simple exercise by conducting the basic Zonation analysis. Let us think that there is a remote country which is the home of seven rare species. We have been given a task to create a proposal for conservation network that will help to protect them. However, due to cost restraints the proposed conservation areas cannot be larger than 15% of the landscape. We decide to use the Zonation program to identify areas that have high priority for conservation. We also decide to use core-area Zonation as our planning method variant, because it best corresponds to our planning objectives (see section 2.3).

In your first species list file (**splist.spp**) you have a list of seven species distribution maps and species-specific parameters in front of the map names. Here all species are given an equal weight, but they have different dispersal α –values, as the use of surrounding landscape (e.g. home ranges) differs between the species. Because no other features are used in this exercise, the last three parameters are given a dummy value of 1. In your first run settings file (**set.dat**) you can find all necessary parameters to run the basic core-area Zonation. If you are operating the program from the windows interface, remember to adjust the settings identical to those found in set.dat -file. To run the analysis, you can call the program yourself or just use the batch file (**do_zig2.bat**) that comes together with the installation package. You can run the batch file from Windows by double clicking it. If you are using Zonation windows interface, just press the "Run"-button. Note that the batch file is a text file that can be edited using notepad. The outcome of this analysis should look like this:

Batch file: do_zig2.bat

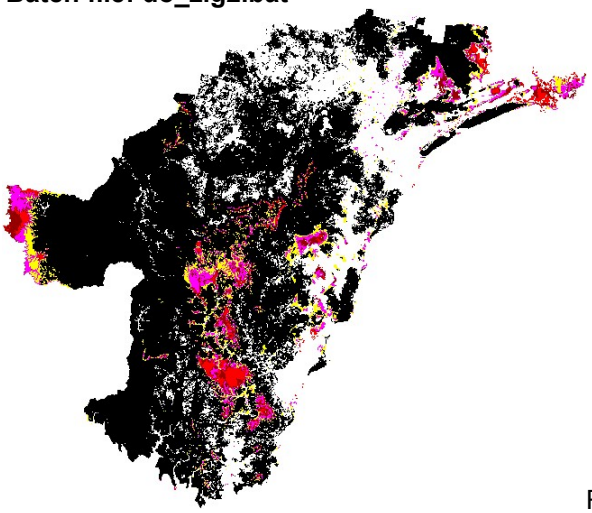


Rank = 1.0

As you remember, the biologically most valuable areas are shown here as red. Since we have the restriction of 15% on the area that we can protect, we now have to find those areas that compile the best 15% of the landscape. Thus, enter the target value (0.15) into the "Rank" -field and press the button. The program will now show you the top 15% fraction of the landscape for all species. Check also how large an area would be needed to protect at least 30% of all species distribution ("Remaining" -button). Double-clicking the image lets you save it into a graphics file. Remember also that the information used to produce these figures has been saved into the .rank.asc and .prop.asc files, which you can import into GIS to prepare your own figures.

© 2004-2006 Atte Moilanen

Batch file: do_zig2.bat



Rank = 0.15

Remaining 30%:	Top 15%:
Area = 27 582	Area = 16 543
BL/A = 0.587	BL/A = 0.971
Cost = 27 582 (cells)	Cost = 16 543 (cells)
av. prop. = 33.0%	av. prop. = 20.6%
min. prop = 29.9%	min. prop = 18.3%

The cell ranking is only one half of the relevant Zonation output. The other half is a set of curves describing the absolute performance levels of species. The figure below shows the minimum (red line) and average (blue line) performance across species for our basic Zonation analysis above. With this data a fraction of species distributions is lost already when only a small fraction of the landscape has been removed. This reflects the fact that the species in the sample data are both relatively widespread and that some of them have mostly non-overlapping distributions. (This is different from, e.g., the analysis of British butterflies, where the distributions of species were narrow and nested, and a substantial fraction of species distributions could be covered with 10% of the landscape. See Moilanen et al. 2005.) The data for generating these curves, and the respective species-specific curves, is output into a .curves.txt file.

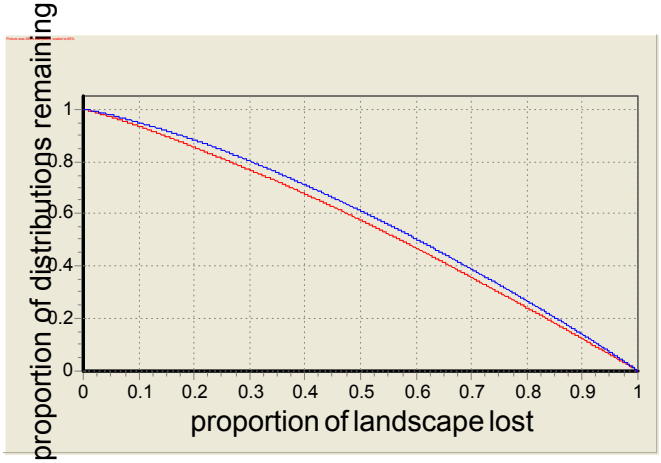


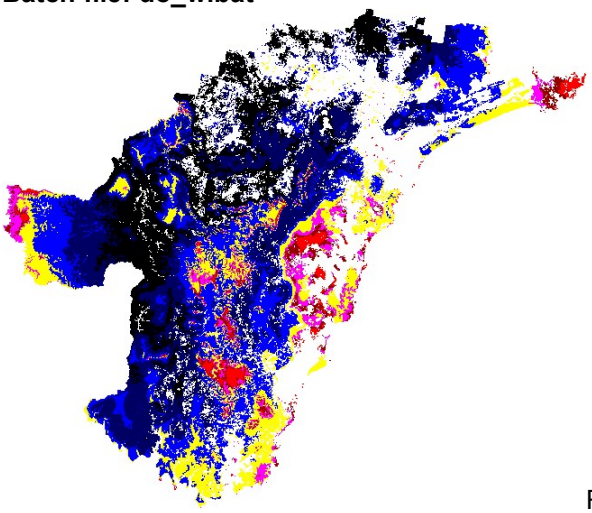
Figure showing how the average and minimum proportions of species distributions are declining as landscape is removed.

© 2004-2006 Atte Moilanen

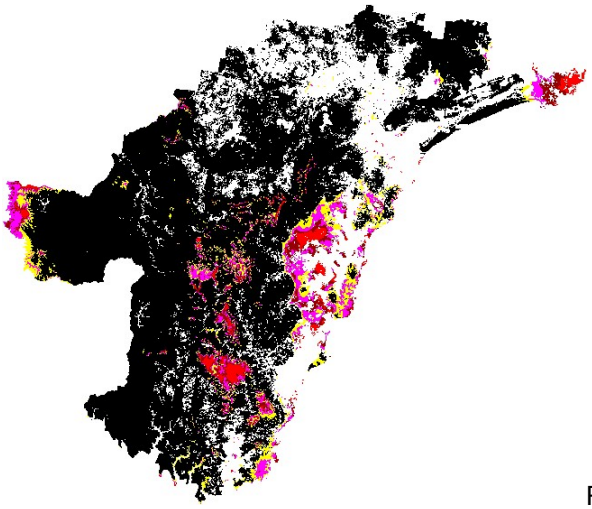
Exercise 2. Weighting of species

Now we have gotten started. However, two of our target species (species 2 and 3) are endemic and can not be found anywhere else in the world. Thus we want to enhance the protection of these species. This can be done by giving each of the species a weight of 2. The weights are determined in the species list file - we now use a different file called **splist_w.spp**. Also the output files need to be renamed (**output_w.txt**) so that the program will not overwrite our earlier solution. The settings file used here is the same as in exercise 1. Use the **do_w.bat** batch file to run the program or call the program yourself. Just remember to rename your output file so the program will not overwrite the solution from the previous exercise.

Batch file: do_w.bat



Rank = 1.0



Rank = 0.15

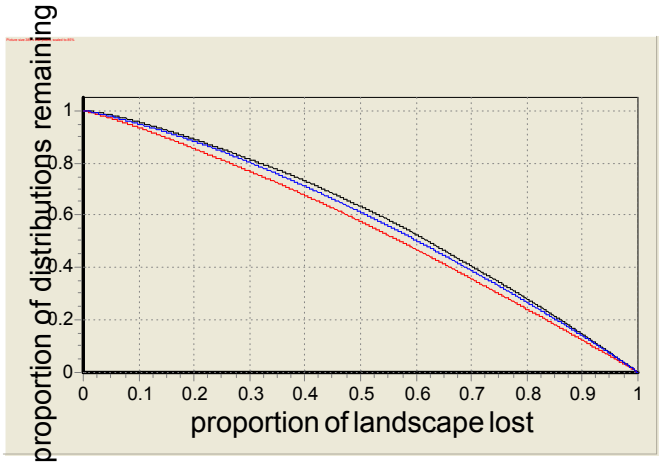
Remaining 30%:
Area = 29 882
BL/A = 0.648
Cost = 29 882 (cells)
av. prop. = 36.5%
min. prop = 29.9%

Top 15%:
Area = 16 543
BL/A = 0.932
Cost = 16 543 (cells)
av. prop. = 20.7%
min. prop = 14.7%

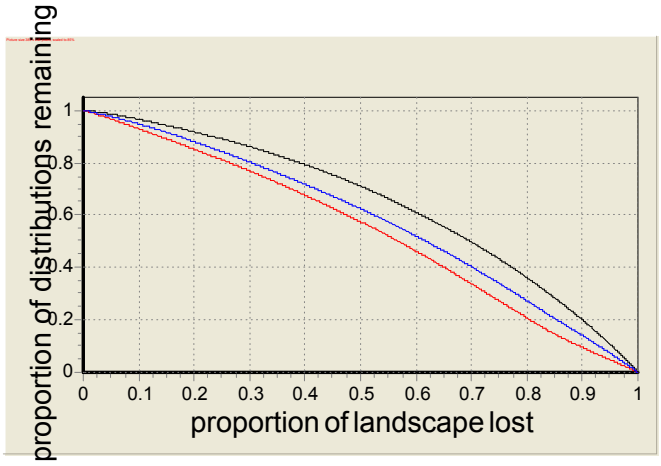
As you see the weighting of species alters the spatial distribution of the highest value cells. Here more importance has been given to the areas where the two endemic species occur (e.g. west and south coast) and less to those areas that have a high representation for the other species (e.g. the peninsula on the east and the north-east region). A difference between the basic and weighted Zonation runs can be seen also in the species distributions curves in the Species info -window.

© 2004-2006 Atte Moilanen

Basic Zonation



Weighted Zonation



If you compare the two solutions, you can find that the relationship between landscape loss and **average** biodiversity protection for all species is quite similar in both cases (blue line). However, when species 2 and 3 are weighted, they retain a relatively higher proportion of their distributions through the cell removal process compared to the basic Zonation run where no weights are used. In turn the minimum proportion retained (species that has the lowest protection) is smaller when using species weighting. The two graphs above show the differences for species 2 (black line) between basic and weighted solution.

Solution comparison (see section 3.6.3) is a useful feature that can be used for visually comparing differences between two solutions. The figure below shows the overlap and differences in the best 15% of landscape between the basic and weighted Zonation runs. Overlapping regions are shown in yellow and areas that are in only one of the solutions are in green (dark green: no weights - light green: weighted).

© 2004-2006 Atte Moilanen

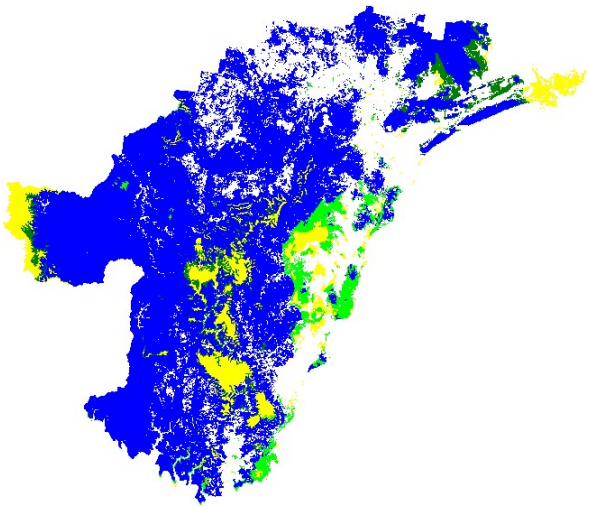


Figure showing differences in top 15% fraction between the non-weighted and weighted solution.

Exercise 3. Adding aggregation into the analyses

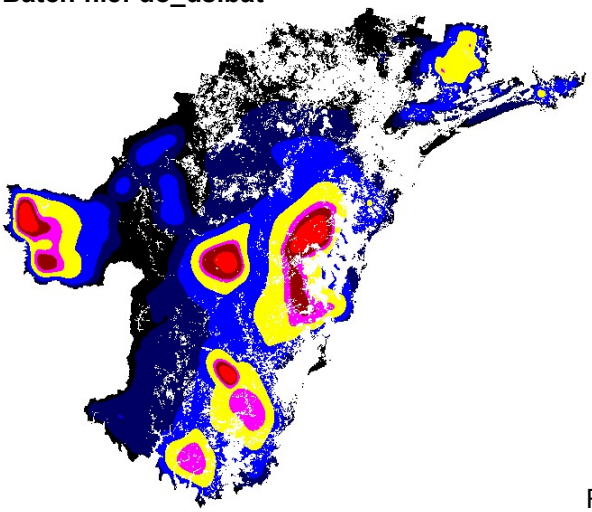
Now we have identified sites that have a high occurrence of our target species (weighting the two endemic species). But the areas are quite fragmented, which is never a good quality in a reserve network. Thus we want to produce a more aggregated solution.

To do this we try two different aggregation methods, **distribution smoothing** and the **boundary quality penalty**. Both methods favour the selection of contiguous cell groups, rather than selecting more fragmented sets of cells. This in turn offers advantages in terms of greater connectivity, and can also promote more practical and cost-effective management. Note that it is not recommended to use several aggregation methods simultaneously due to difficulties in interpreting the results.

3a. Distribution smoothing

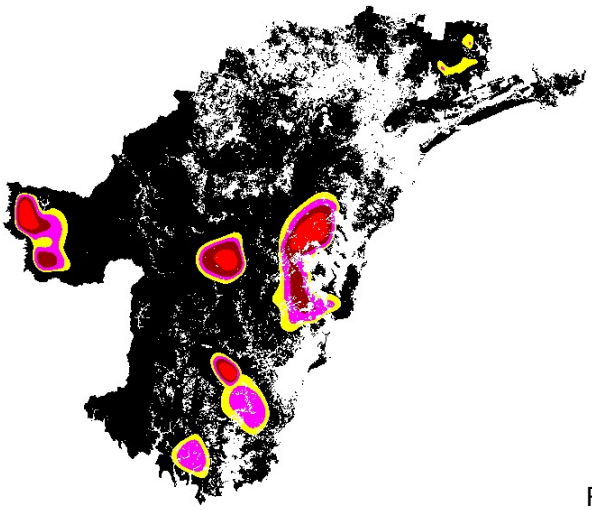
Using this method results more aggregated solutions based on the connectivity of sites. To add the distribution smoothing to the analysis we use the same input files as in exercise 2, but we call the program with a new batch file, **do_ds.bat**. Note that the species-specific smoothing is defined in the species list file, where the width of the smoothing kernel for each species is defined in the 2nd column, and in the call itself, where the third last parameter (value = 1) indicates that distribution smoothing will be done.

Batch file: do_ds.bat



Rank = 1.0

© 2004-2006 Atte Moilanen



Rank = 0.15

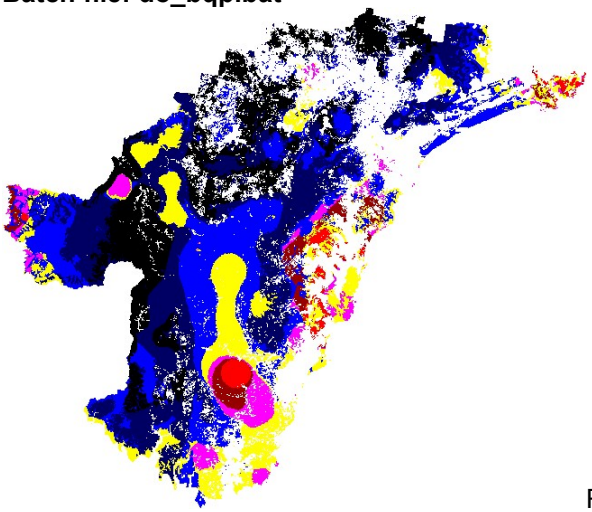
Remaining 30%:
Area = 27 493
BL/A = 0.205
Cost = 27 493 (cells)
av. prop. = 33.2%
min. prop = 29.9%

Top 15%:
Area = 16 543
BL/A = 0.285
Cost = 16 543 (cells)
av. prop. = 20.8%
min. prop = 18.6%

3b. Boundary quality penalty

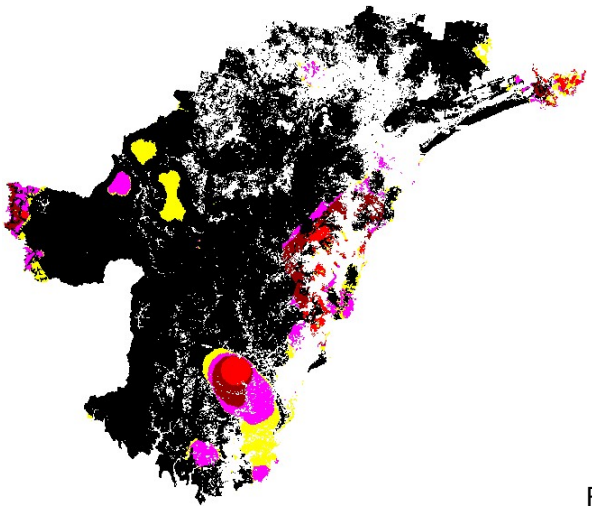
The boundary quality penalty (BQP) calculates the most valuable sites based on both the value of the cell and the effects of habitat loss in the surrounding cells. The effects of fragmentation (loss of neighbourhood cells) are species-specific and thus the BQP also takes in to account how different species are influenced by fragmentation and habitat loss. BQP analysis demands prolonged computation times compared to our previous method, because the loss of a cell now has an effect on occurrence levels in nearby cells, which has to be taken into account in calculations. To include the BQP to our analysis, we now use the settings file **set_bqp.dat**. Because BQP substantially increases computation time, the warp factor has been increased to 500 (in production runs we recommend warp factor of 100 or lower). We also need to use a new species list file, which gives the program all species-specific responses to fragmentation needed for running BQP. Thus use the **splist_bqp.spp** file as species list file. You can use the **do_bqp.bat** file to run the analysis or call the program yourself.

Batch file: do_bqp.bat



Rank = 1.0

© 2004-2006 Atte Moilanen

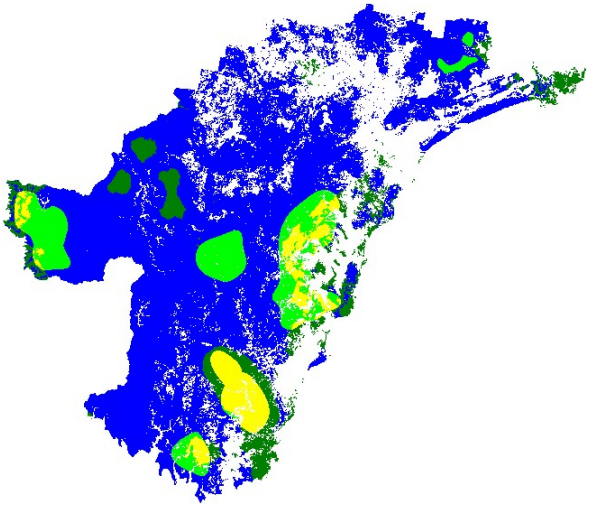


Rank = 0.15

Remaining 30%:
Area = 30 875
BL/A = 0.563
Cost = 30 875 (cells)
av. prop. = 37.8%
min. prop = 29.9%

Top 15%:
Area = 16 543
BL/A = 0.703
Cost = 16 543 (cells)
av. prop. = 21.6%
min. prop = 15.4%

As you see, the two solution are fairly different. To get a better picture of the main differences use the solution comparison. You can either use the top 15% fraction of the two solutions for the comparison (see figure below), or you can check from the results how large fractions were needed to protect the 30% of all species distributions and use these fractions for the comparison.



Comparison between top 15% areas selected by Zonation with distribution smoothing and Zonation using the BQP. Overlapping areas are shown in yellow, light green areas are present only in distribution smoothing solution and dark green areas only in BQP solution.

Exercise 4. Possible gaps in species information

Due to lack of data, uncertainties in species distribution are a common problem encountered in ecological studies. However, these uncertainties can be accounted for in reserve selection when using the Zonation program. Conceptually, the program uses uncertainty analysis to focus on sites where the prediction uncertainties are low compared to the predicted representation levels. Thus the program prioritizes sites that have a high abundance and low uncertainty.

© 2004-2006 Atte Moilanen

To continue with our exercise, let us think that our species distribution data has been provided by statistical species distribution models (a.k.a. habitat models or resource selection functions, for more detailed information see Elith *et al.* 2002). Models contain many uncertainties in their predictions and we want to take this into account when we are selecting the best sites to be protected. The pair of figures below shows as an example the distribution and its error surface for one species.

Distribution layer for species 2 Uncertainty layer for species 2

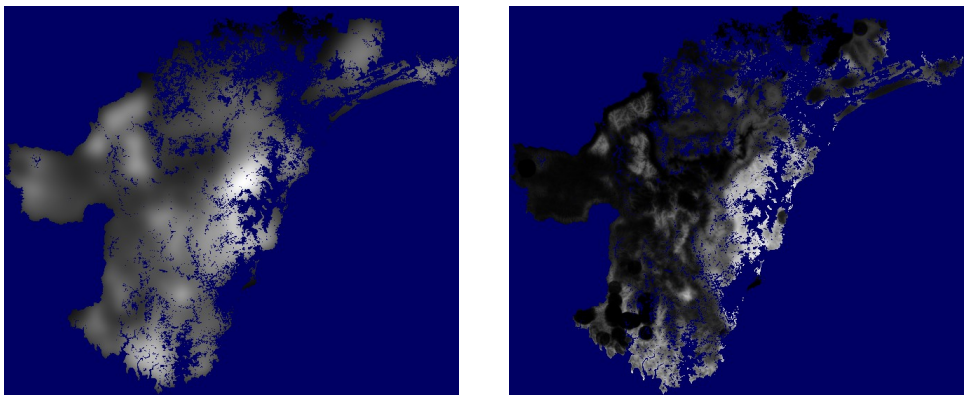
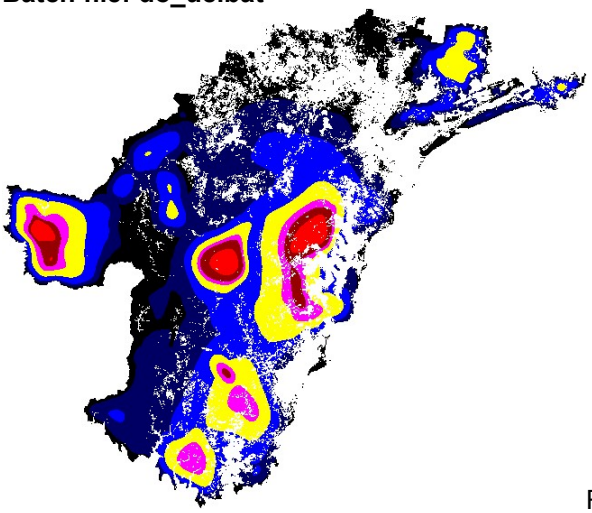


Figure showing the distribution of species 2 and its corresponding uncertainty layer. White indicates high occupancy levels or high error, and black low occupancy or low error. You can display these maps by selecting the species from the pull-down list **in the map window** (for viewing the uncertainty layer remember to select the "Wmap" -option). Save by double-clicking on the image.

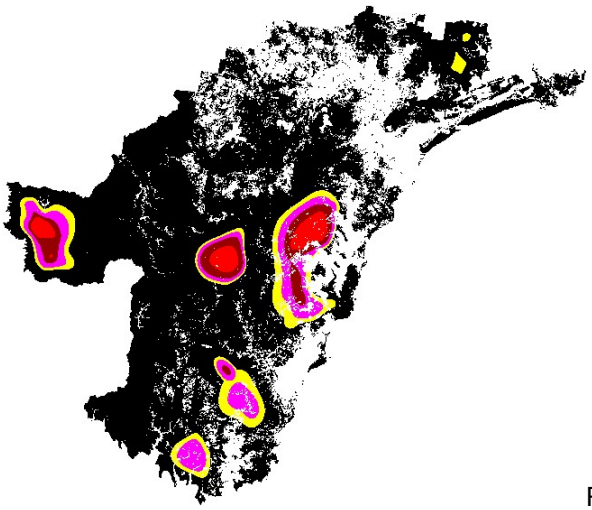
We have uncertainty layers for each of the species (**sp1_UC.asc**, **sp2_UC.asc** etc.), which show the spatial distribution of uncertainty in our data. All uncertainty layers are listed in the **UCweights.spp** -file, where you can also find the species-specific uncertainty weights. In this exercise we want to stress the certainty of data equally for all species, thus we give them an identical weight of 1. We use the same species list file as in exercise 3a, but the settings file needs to be changed to **set_uc.dat**. Again, use the **do_uc.bat** batch file to run the program or call the program yourself. In this exercise, where uncertainty analysis is done together with distribution smoothing, the program first calculates each cell a new value based on the uncertainties in the data and then uses these values for the aggregation part.

Batch file: do_uc.bat



Rank = 1.0

© 2004-2006 Atte Moilanen



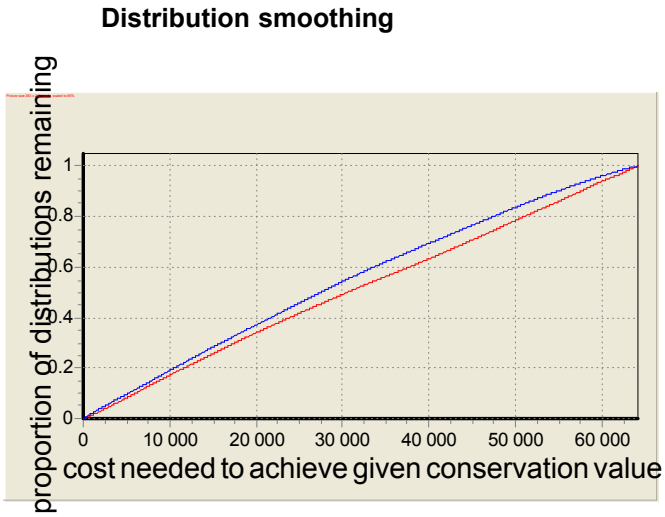
Rank = 0.15

Remaining 30%:
Area = 28 193
BL/A = 0.194
Cost = 28 193 (cells)
av. prop. = 32.9%
min. prop = 29.9%

Top 15%:
Area = 16 543
BL/A = 0.273
Cost = 16 543 (cells)
av. prop. = 20.1%
min. prop = 18.1%

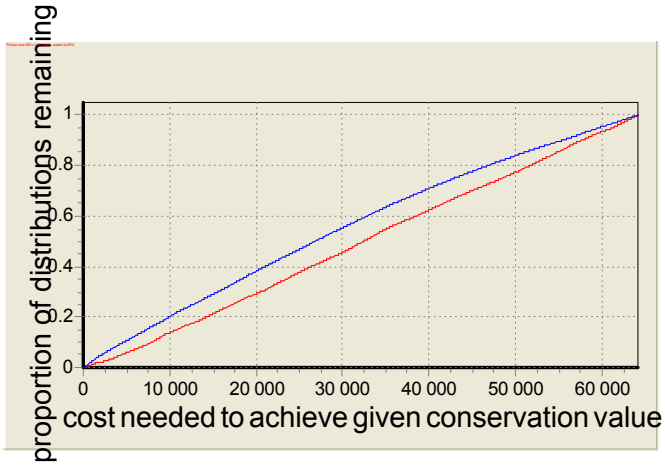
Exercise 5. What about the costs?

As in many cases in conservation biology, costs play a vital part in reserve planning. So far we have been looking for sites based solely on their biological value and ignoring the possible costs. But, assume that in our study area land is most expensive at the south-west and cheapest at the north-east region. Now we need to determine how much the protection of our proposed areas would actually cost. We will do this by loading the two solutions calculated in exercise 4 with a cost layer (**cost.asc**). This way the program can calculate the increase of cost as cells are removed in the exact same order as they were when producing the solutions in the previous exercise. Use the two batch files, **load_costds.bat** and **load_costbqp.bat**, to see how large differences, if any, there is in the land costs between the two solutions.



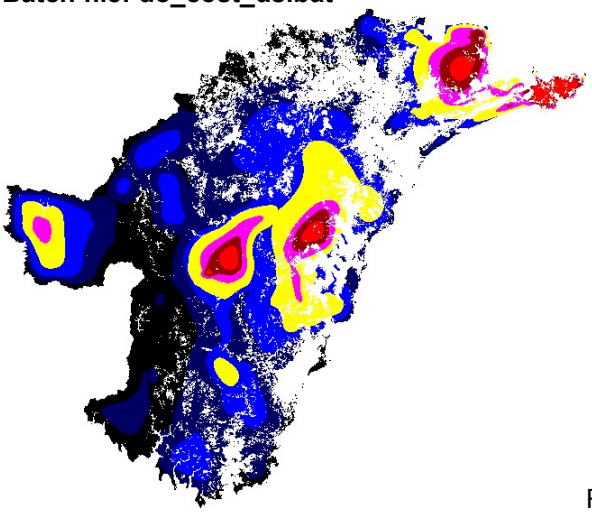
© 2004-2006 Atte Moilanen

Boundary Quality Penalty



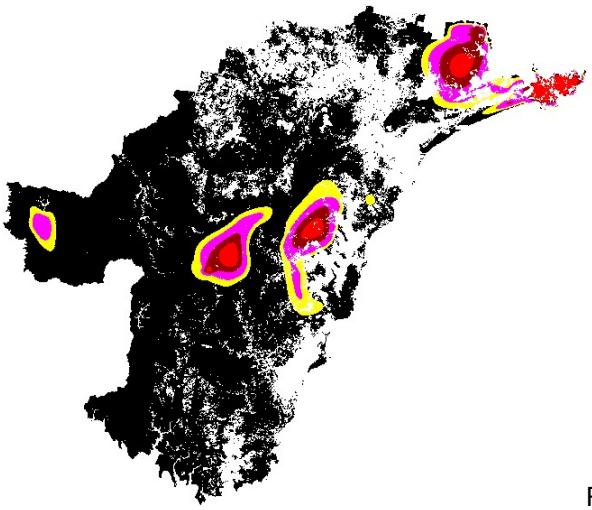
Another possibility would be to include the cost into the analyses during the cell removal process. This way the program would calculate a solution that has both high conservation value and low demands for resources. This is achieved by selecting cells that have a high conservation value/cost ratio. To do this we rerun the analysis using a cost layer (instead of loading it with the cost layer, as we did above). Again, we use distribution smoothing as our aggregation method, but you can choose other aggregation methods as well. The run settings for this exercise are defined in **set_costds.dat** -file. Use the **do_cost_ds.bat** -batch file to run the analysis. How do the most important areas change compared to the solution from exercise 3? Compare also the species distribution curves of the two solutions, what changes do you see?

Batch file: do_cost_ds.bat



Rank = 1.0

© 2004-2006 Atte Moilanen



Rank = 0.15

Remaining 30%:
Area = 37 682
BL/A = 0.717
Cost = 18 737 (cells)
av. prop. = 36.7%
min. prop = 29.9%

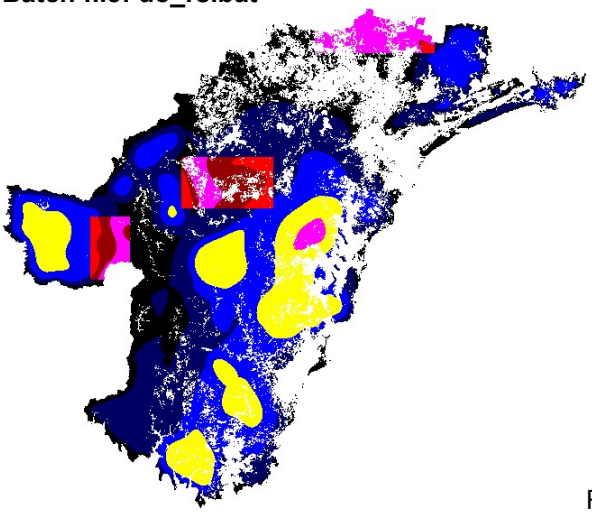
Top 15%:
Area = 16 543
BL/A = 0.329
Cost = 7 411 (cells)
av. prop. = 16.8%
min. prop = 11.0%

Exercise 6. What about the already existing reserves?

When it comes to reserve network planning, managers seldom have the change to start from a fresh table. In many cases the target area already includes older reserves or areas that are ear-marked for other land uses such as agriculture, forestry or habitation etc. Thus, one often has to take into consideration areas that either can not be included or need to be included into the reserve network. Let us think that our example landscape already has a couple of reserves that we have to include to the final solution.

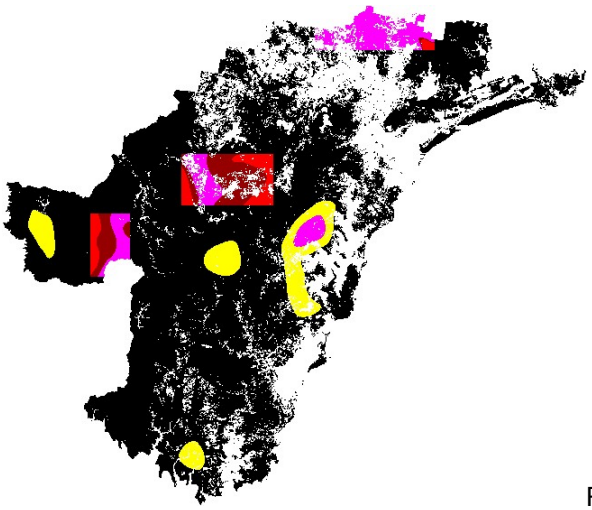
To do this we use the mask option which allows us to classify cells to different categories, which in turn define the cell removal order. In the tutorial package you can find a mask file which includes three reserves (**mask_rs.asc**). We run the analyses once more as in exercise 4, but this time we include the mask (see **set_maski.dat**). Thus call the program with a new batch file **do_rs.bat**.

Batch file: do_rs.bat



Rank = 1.0

© 2004-2006 Atte Moilanen

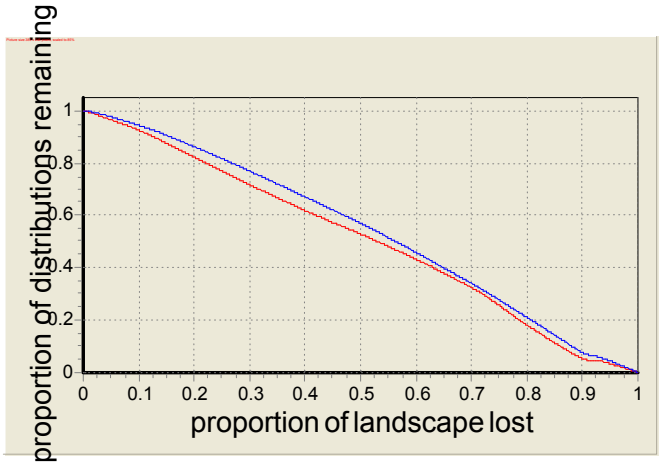


Rank = 0.15

Remaining 30%:
Area = 30 830
BL/A = 0.271
Cost = 30 830 (cells)
av. prop. = 31.6%
min. prop = 29.9%

Top 15%:
Area = 16 543
BL/A = 0.369
Cost = 16 543 (cells)
av. prop. = 14.4%
min. prop = 11.4%

Compare the solution to the results from exercise 4. How has the representation of species altered now that the old reserves are included in the top 15% fraction? Note the differences at the end of the species distribution curves. As you see, the solution received with the old reserves is suboptimal, since the program is forced to include poor quality areas in the top fraction.

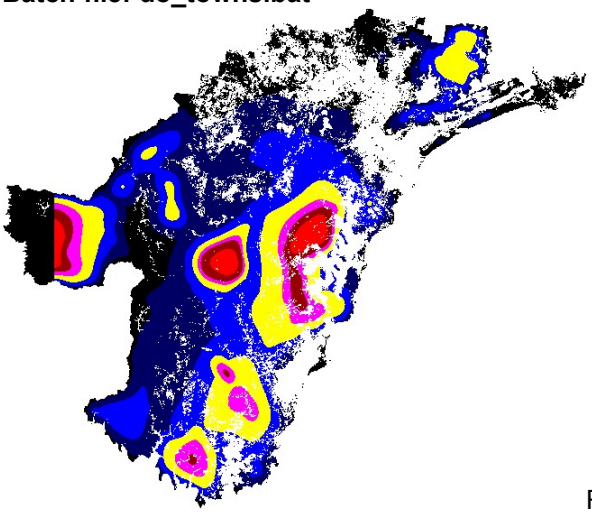


Average and minimum performances when old reserves are included to the top fraction.

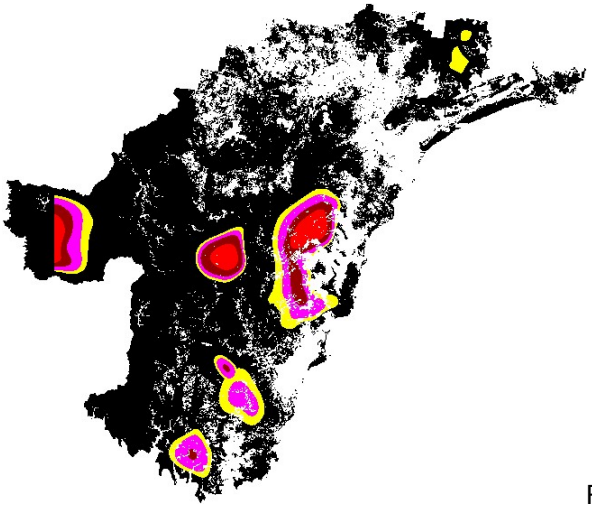
In some cases the situation is the other way around, where areas can not be included to the reserve network for some reason. Thus these areas need to be first masked out from the landscape, before ranking the rest of the area. See how this kind of masking would change the results in our study area by running the analysis with the last batch file, **do_towns.bat**, where we have two imaginary regions marked as residential area (**mask_towns.asc**). In this exercise we use the **set_maske.dat** -settings file, all other input files are identical to the exercise 4.

© 2004-2006 Atte Moilanen

Batch file: do_towns.bat



Rank = 1.0

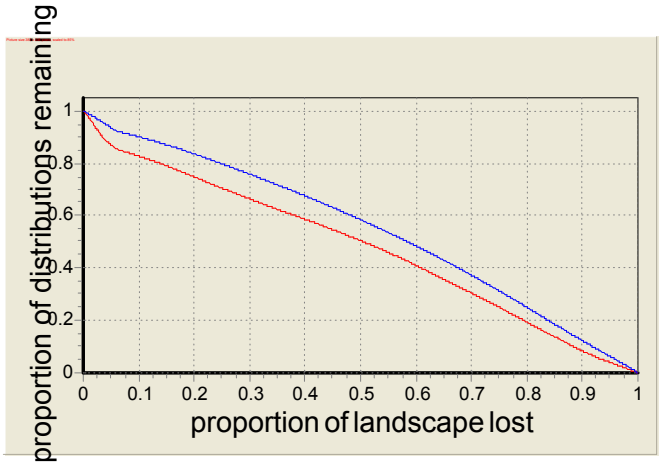


Rank = 0.15

Remaining 30%:	Top 15%:
Area = 32 360	Area = 16 543
BL/A = 0.251	BL/A = 0.281
Cost = 32 360 (cells)	Cost = 16 543 (cells)
av. prop. = 36.5%	av. prop. = 19.7%
min. prop = 29.9%	min. prop = 16.6%

This time you can see the changes in the beginning of species distribution curves. Since the two excluded areas have high biological value, the proportions of species distributions decrease more steeply in the beginning when these areas are removed. However, since other valuable areas can be included in the solution, this masking has less effect on the final 15% top fraction compared to the old reserves, as you can see from the average and minimum proportions of species distributions.

© 2004-2006 Atte Moilanen



Average and minimum performances when residential areas are excluded from the top fraction.

As a final word, this tutorial does not include all variants of everything. When working with your own data, remember to carefully consider the cell removal rule you use. Analysis options that you might well wish to modify include edge removal, the warp factor, and adding of fake edge points. See sections 3.5 and 3.6 for a full list of options.

© 2004-2006 Atte Moilanen

Index

- A -

adding edge points 42
additive benefit function 14, 15
aggregation methods 19
aim & purpose 4
alfa value 39
algorithm 13
annotations 50
assumptions 31, 83

- B -

basic core-area Zonation 14
batch files 35
batch runs 35
boundary length penalty 23
boundary quality penalty 21, 61
boundary quality penalty definitions file 48
BQP mode 42
bugs 83

- C -

call 33
cell removal rule 14, 17
colors 50
command line 33
command prompt 33, 81
compulsory input files 38
cost curves 50
costs 45
curves 50
curves file 55

- D -

dirstibution discounting 63
distribution curves 50
distribution discounting 25, 47, 48
distribution smoothing 20, 59
distributional uncertainty map layer 47

- E -

edge removal 42
error weights 48
errors in data 25
examples 85
excluding areas from the solution 28, 66
extinction risk curve 50

- F -

fragmentation uncertainty analysis 27, 75
frame work 5

- H -

horizon of uncertainty 25, 63

- I -

including areas to the solution 28, 66
initial removal 42
Input files 37, 38, 45
installation 8

- K -

known software problems 83

- L -

landscape identification 69
landscape statistics 72
limitations 31, 83
loading old solutions 37, 80
logit space 42

- M -

management landscapes 69, 72
map colors 50
map layout 50
maps -window 50
mask layer 46
memo -window 50
multiple batches 35

© 2004-2006 Atte Moilanen

- N -

name annotation 42

- O -

optional input files 45
output 50
output files 55
overlap in landscapes 73

- P -

Pareto-optimal boundary 25
penalty curves 48
post-processing analyses 69
printing options 50
proportional error 42
proportional loss file 55
proportional selection 50

- Q -

quick start 8

- R -

ranking file 55
ranking map 50
rarity map 50
references 12
remaining map 50
replacement cost analysis 28, 46, 66
richness map 50
robustness of solutions 25
run info file 55
run settings 42
running basic Zonation 57
running the program 33, 34

- S -

scale of landscape use 39
selection frequency 77
settings 34
solution comparison 73
species distribution map files 38
species info -window 50
species list file 39
species-cell-specific errors 47
surrogate species 57
system requirements 83

- T -

target-based planning 14, 16
testing old solutions with new settings 80
troubleshooting 81
tutorial 85

- U -

uncertainty analyses 24
uncertainty analysis weights file 48
uncertainty parameter 25, 63
uniform error 42
using command prompt 81

- W -

warp factor 42
weighting 57
weights 39, 57
weights in uncertainty analysis 48
windows interface 34
visual output 50

- Z -

ZIG-sum utility 77
Zonation compared to other reserve selection approaches 5
Zonation features 5
Zonation meta-algorithm 13
Zonation work flow 7
z-value 42

© 2004-2006 Atte Moilanen

For the newest version of Zonation software, check out the MRG web site:

www.helsinki.fi/science/metapop/

Contact information

Metapopulation Research Group
Department of Biological and Environmental Sciences

P.O. Box 65 (Viikinkaari 1)
FI 00014 University of Helsinki
FINLAND

Phone: +358 9 1911 (Exchange)
Fax: +358 9 191 57694